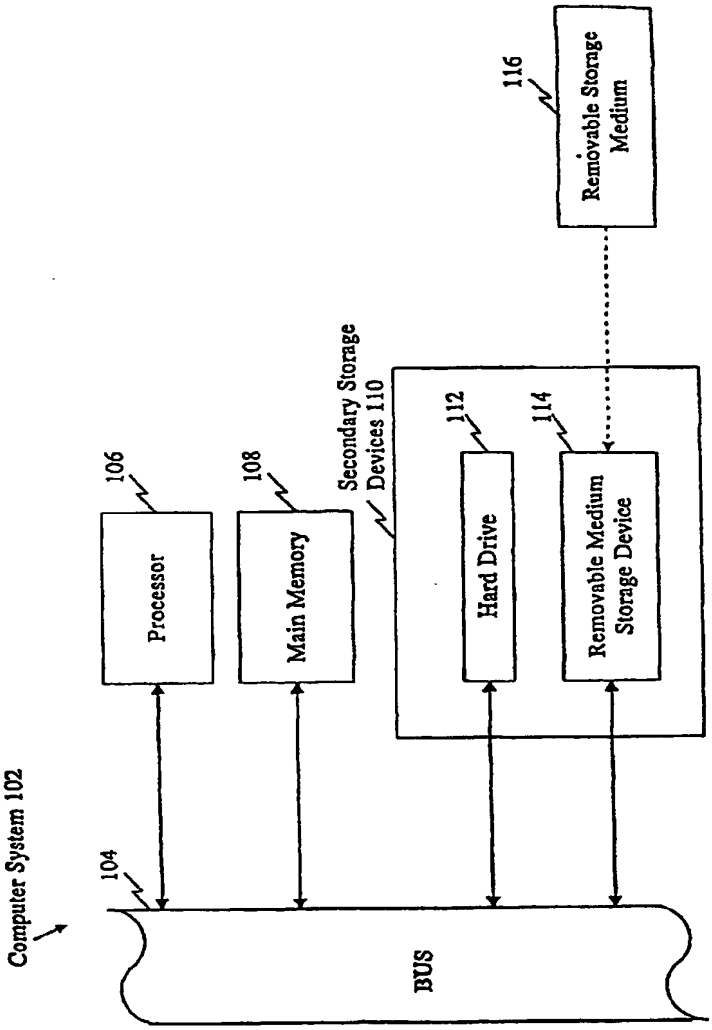

116
Removable Storage Medium
Secondary Storage Devices 110
112
114
106
108
Processor
Main Memory
Hard Drive
Removable Medium Storage Device
Computer System 102
104
BUS

FIGURE 1

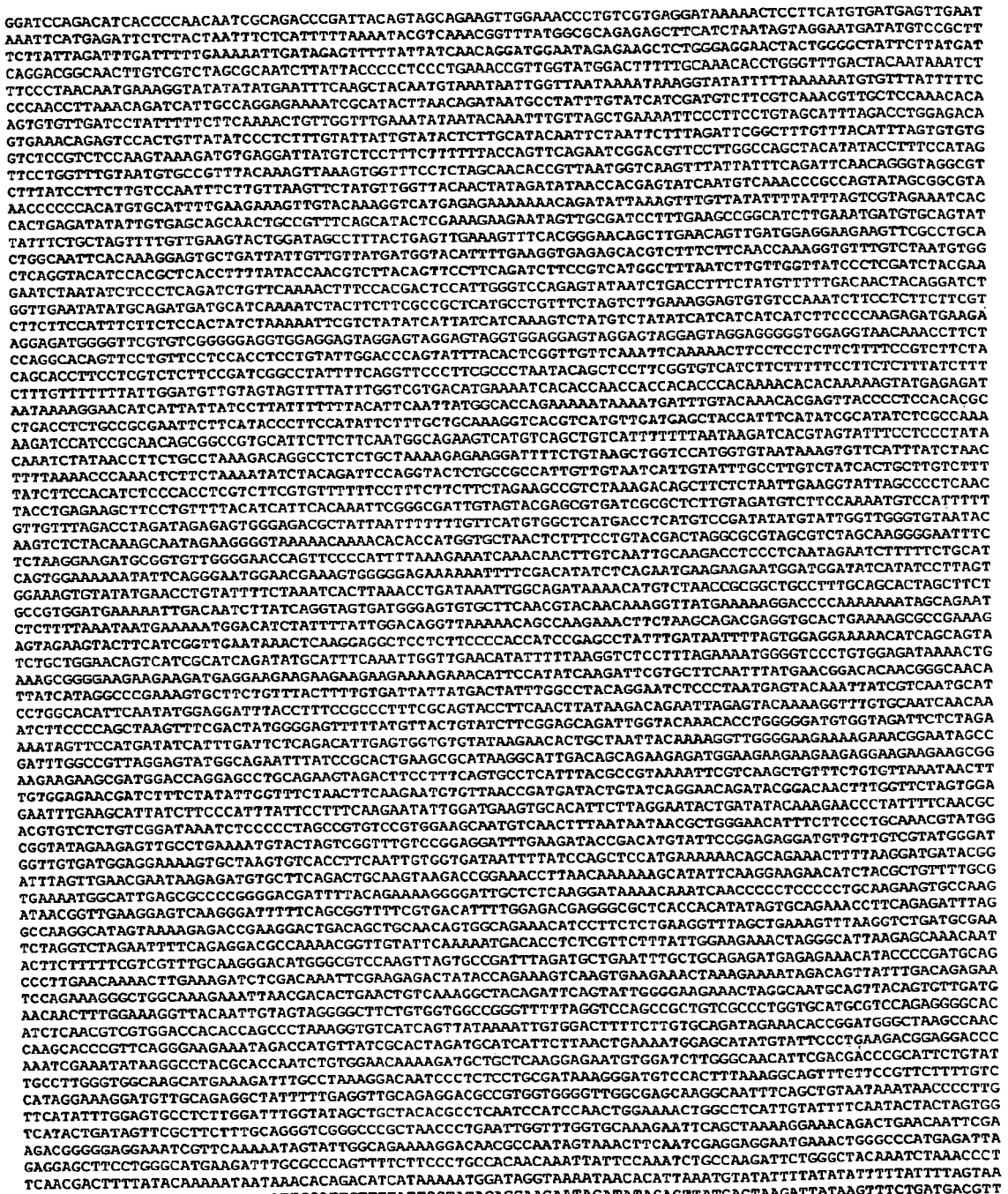


FIGURE 2, Sheet 1 of 40

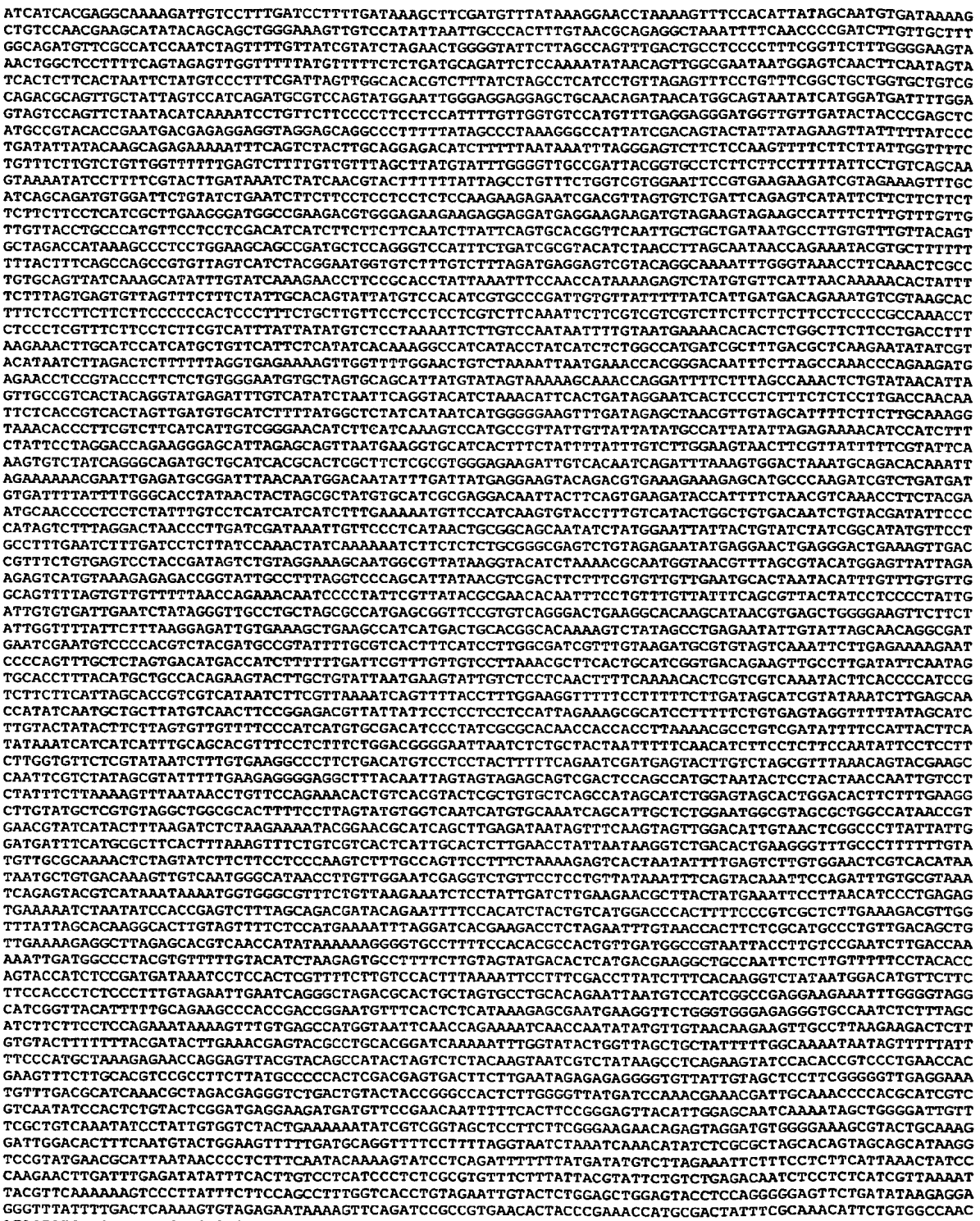


FIGURE 2, Sheet 2 of 40

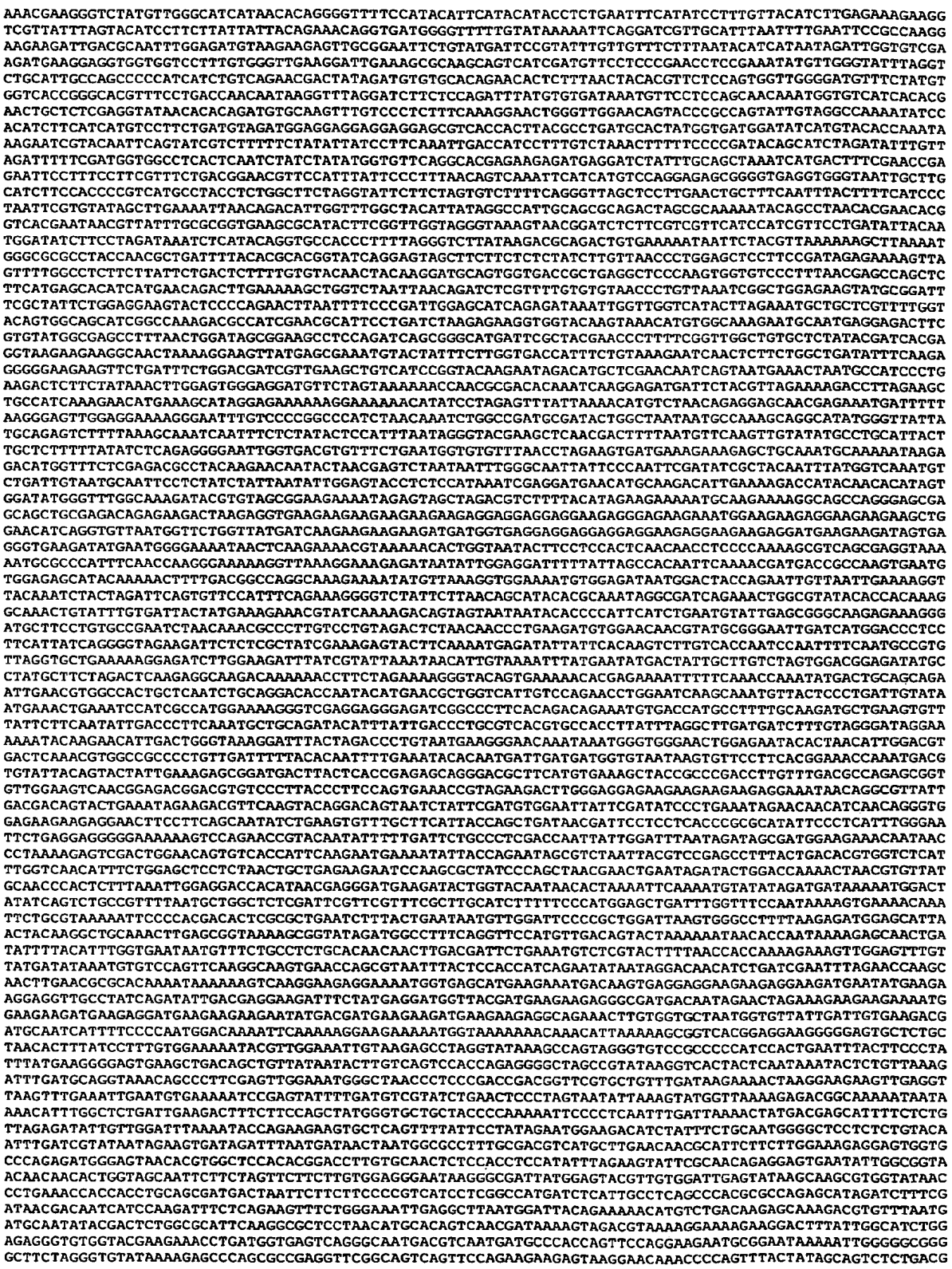


FIGURE 2, Sheet 3 of 40

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FIGURE 2, Sheet 4 of 40

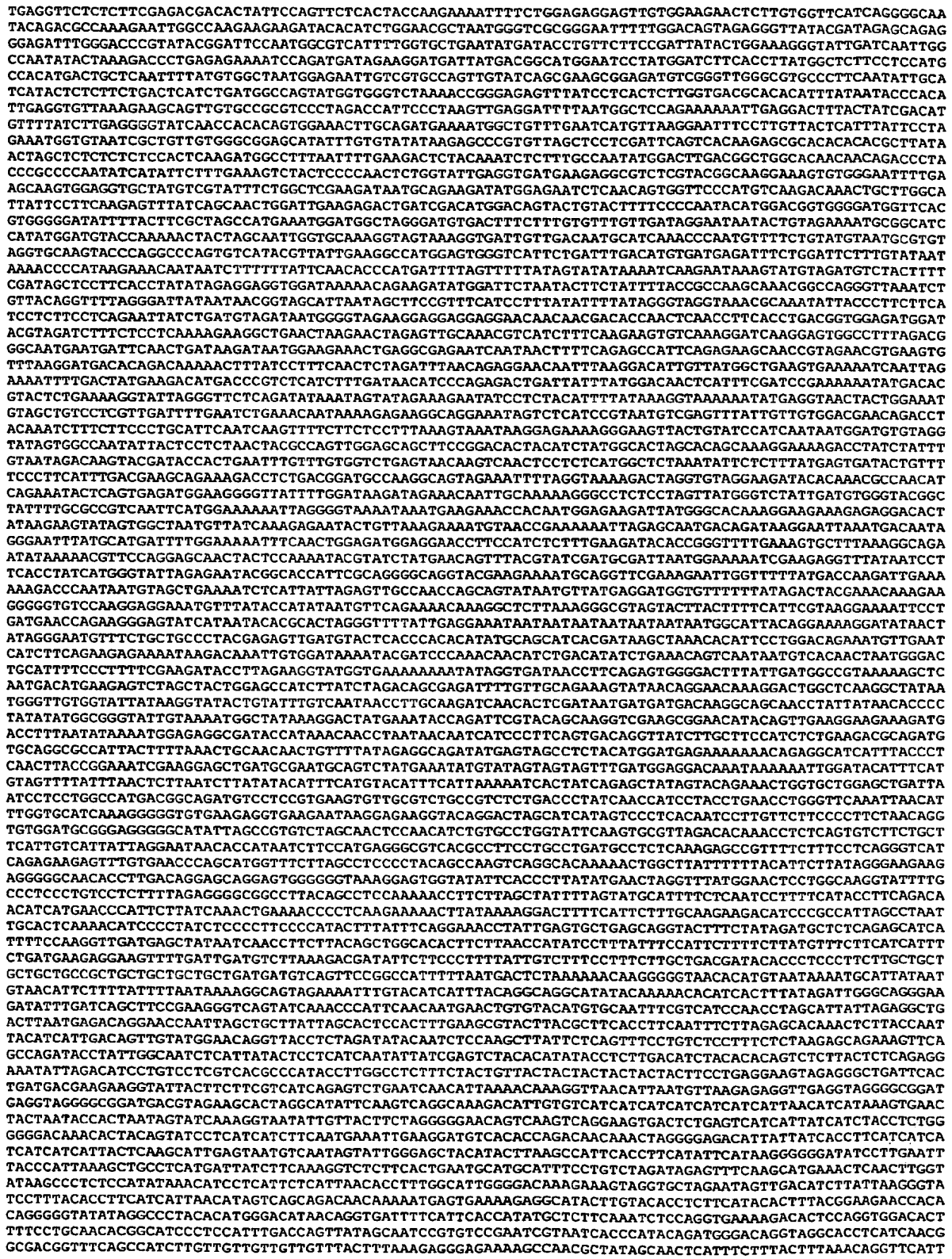


FIGURE 2, Sheet 5 of 40

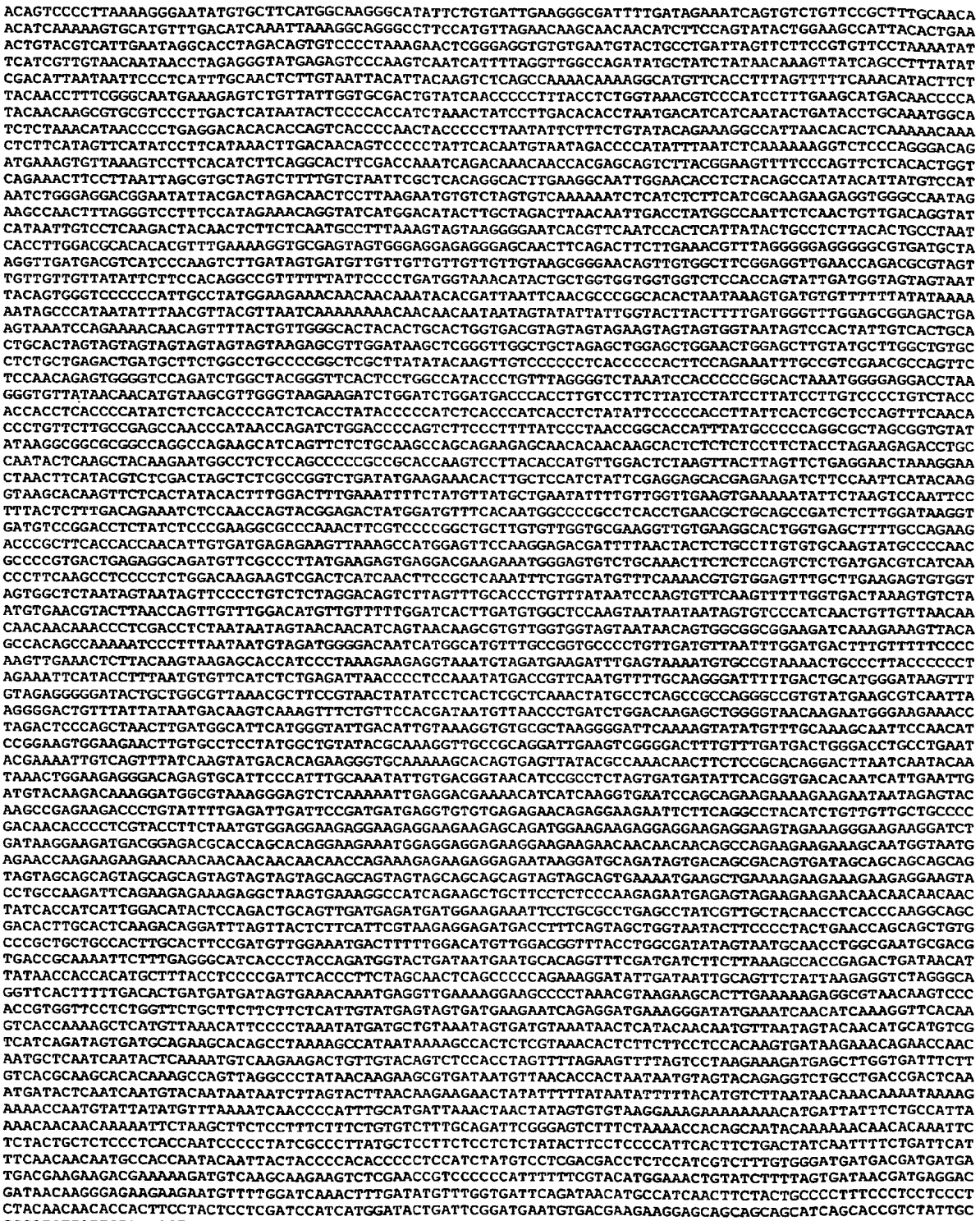


FIGURE 2, Sheet 6 of 40

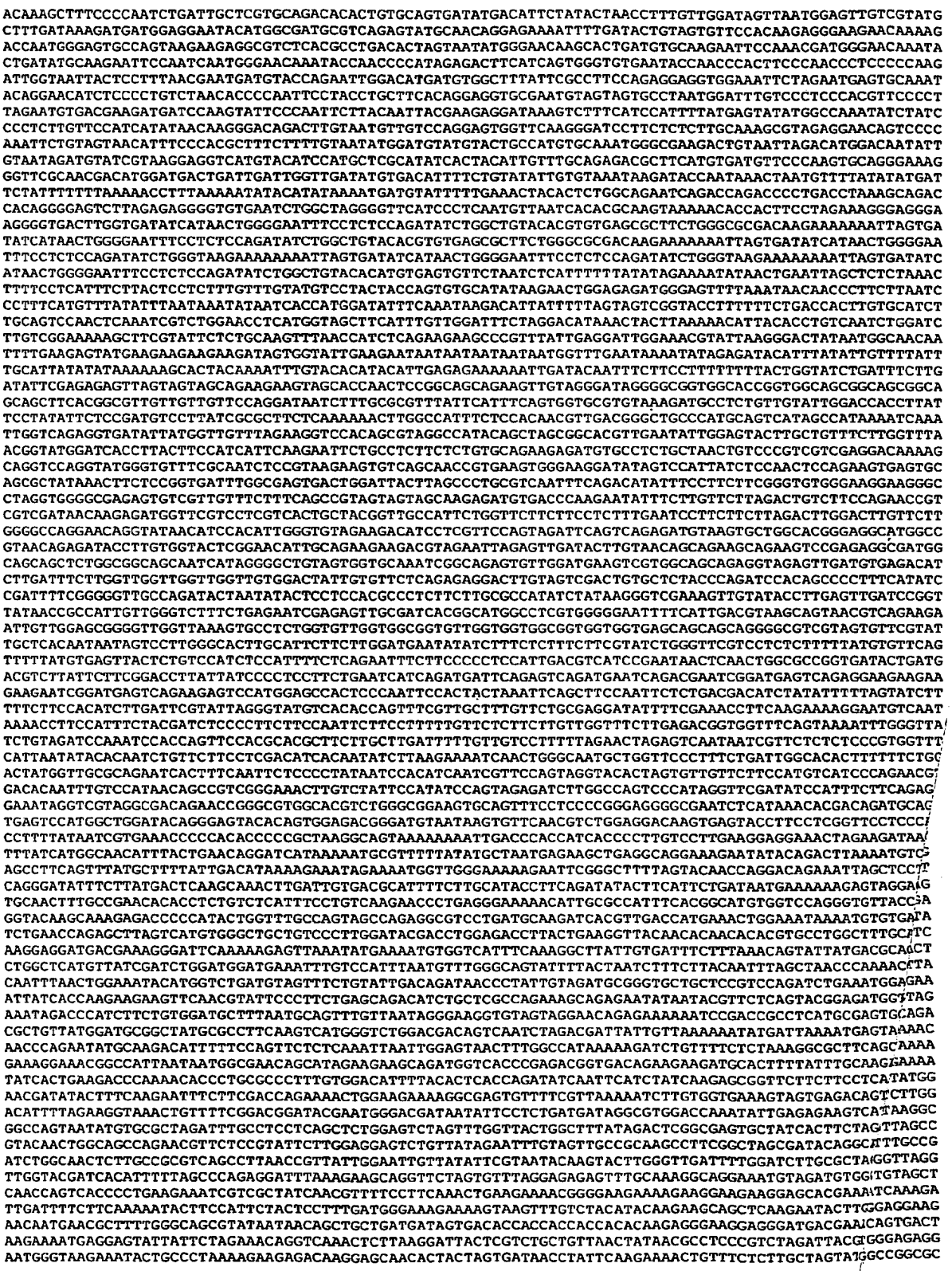


FIGURE 2, Sheet 7 of 40

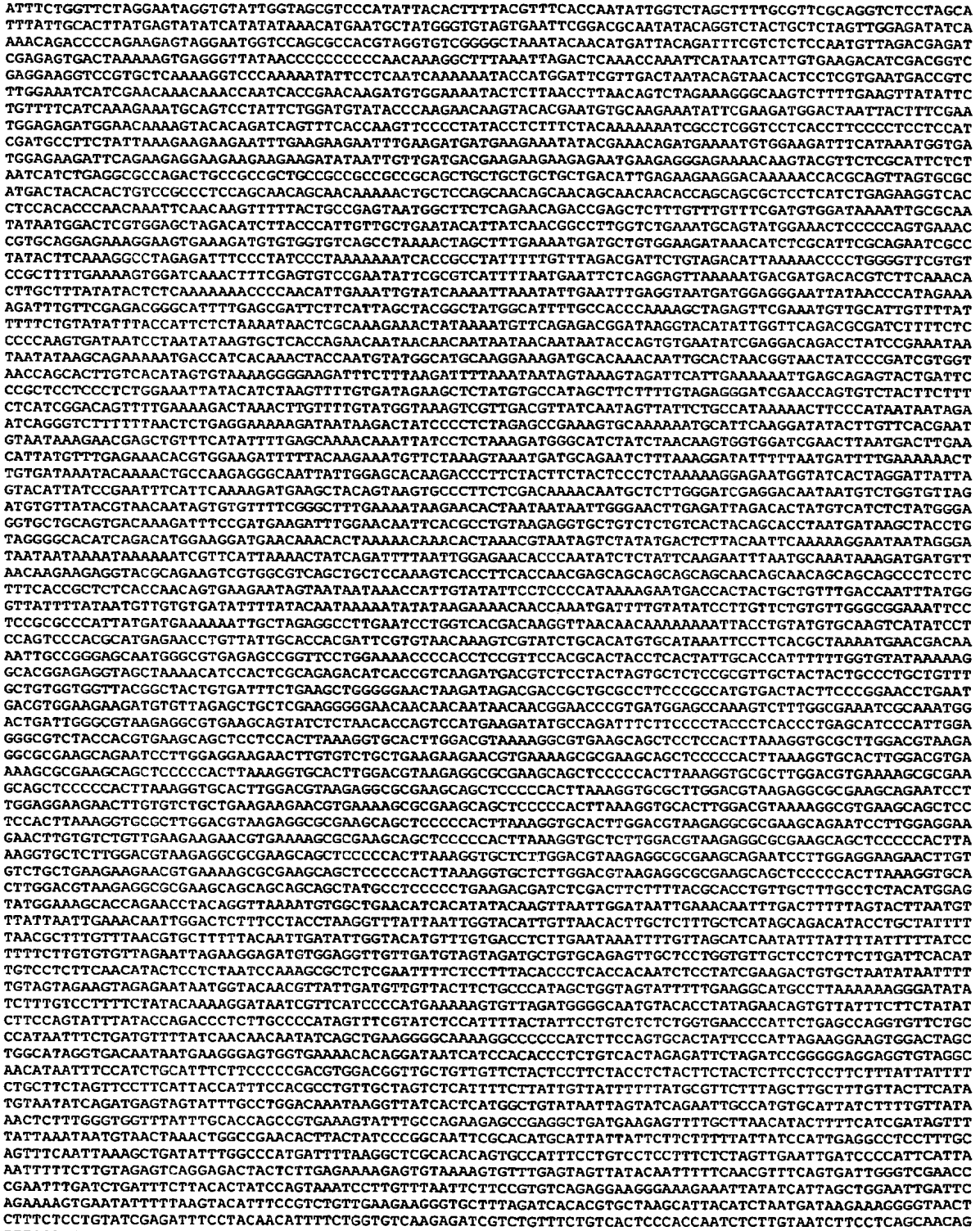


FIGURE 2, Sheet 8 of 40

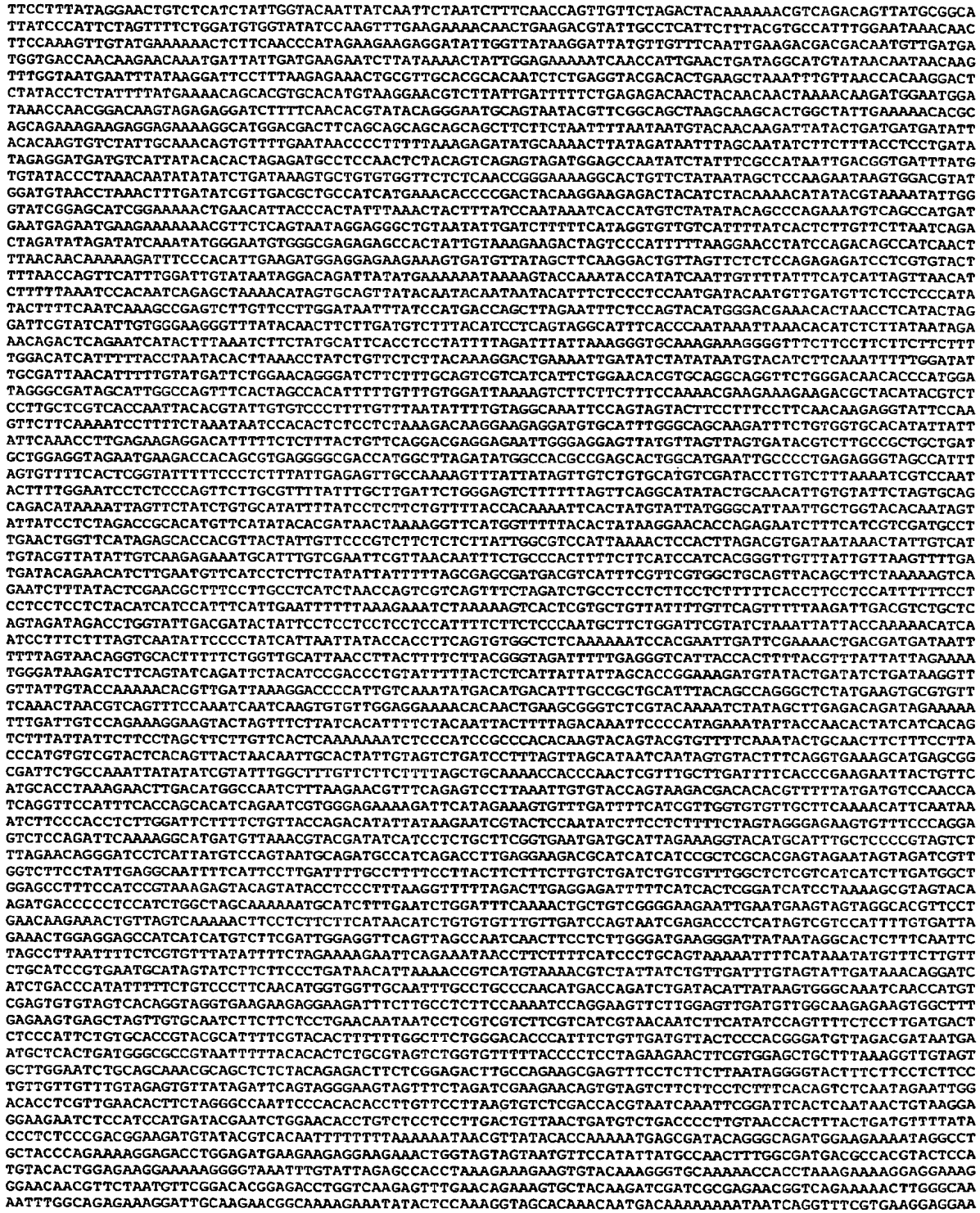


FIGURE 2, Sheet 9 of 40

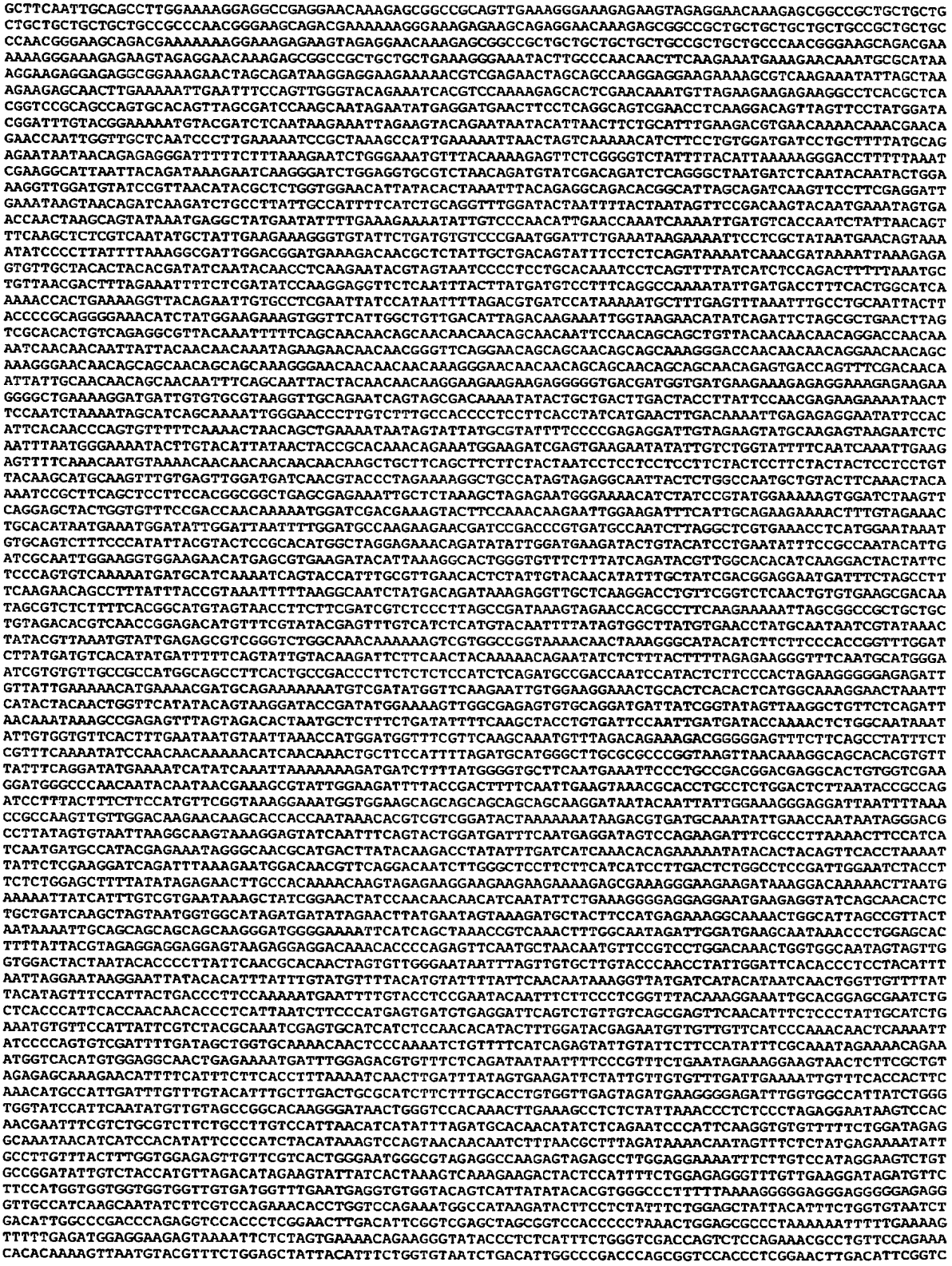


FIGURE 2, Sheet 10 of 40

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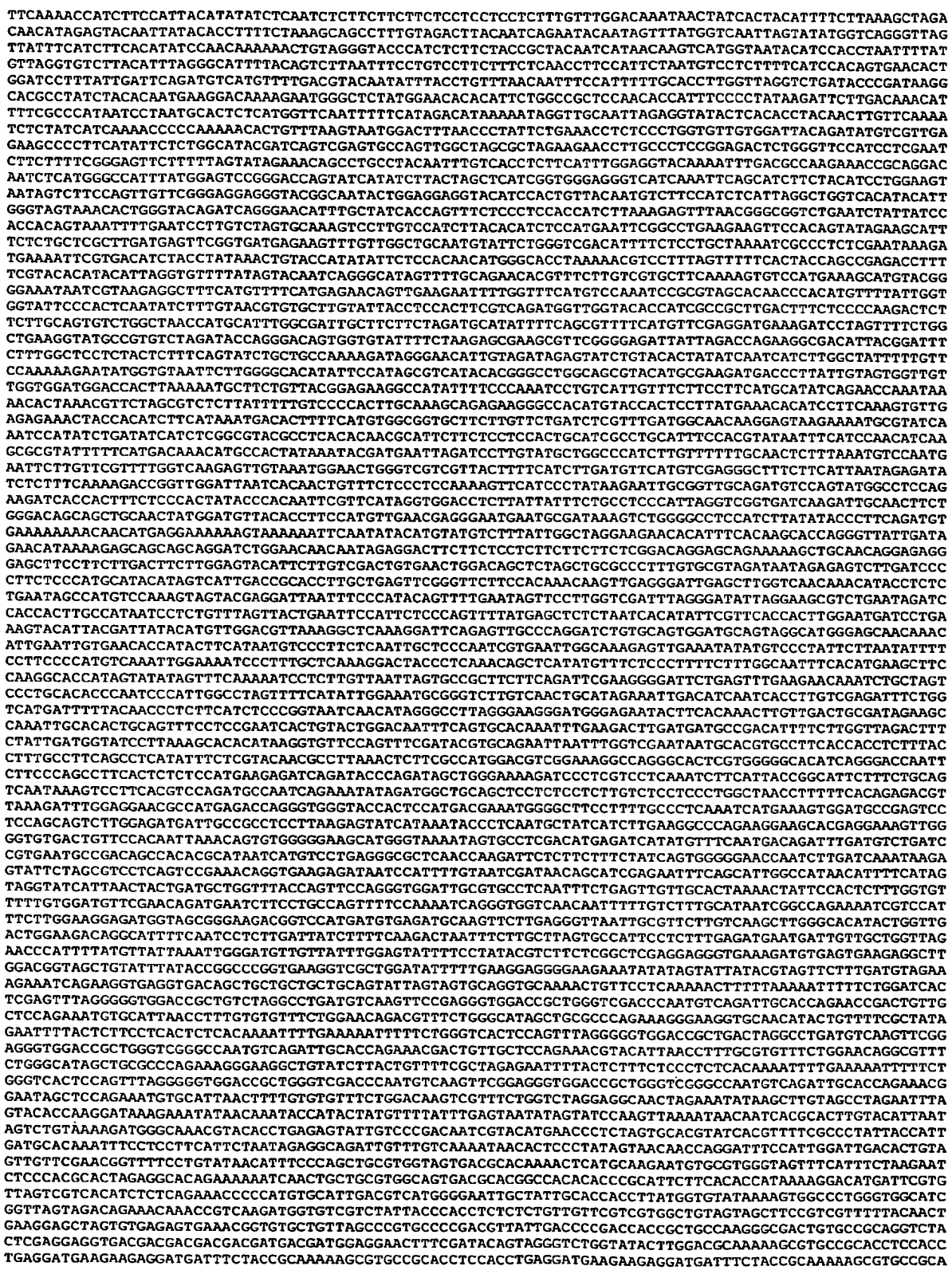


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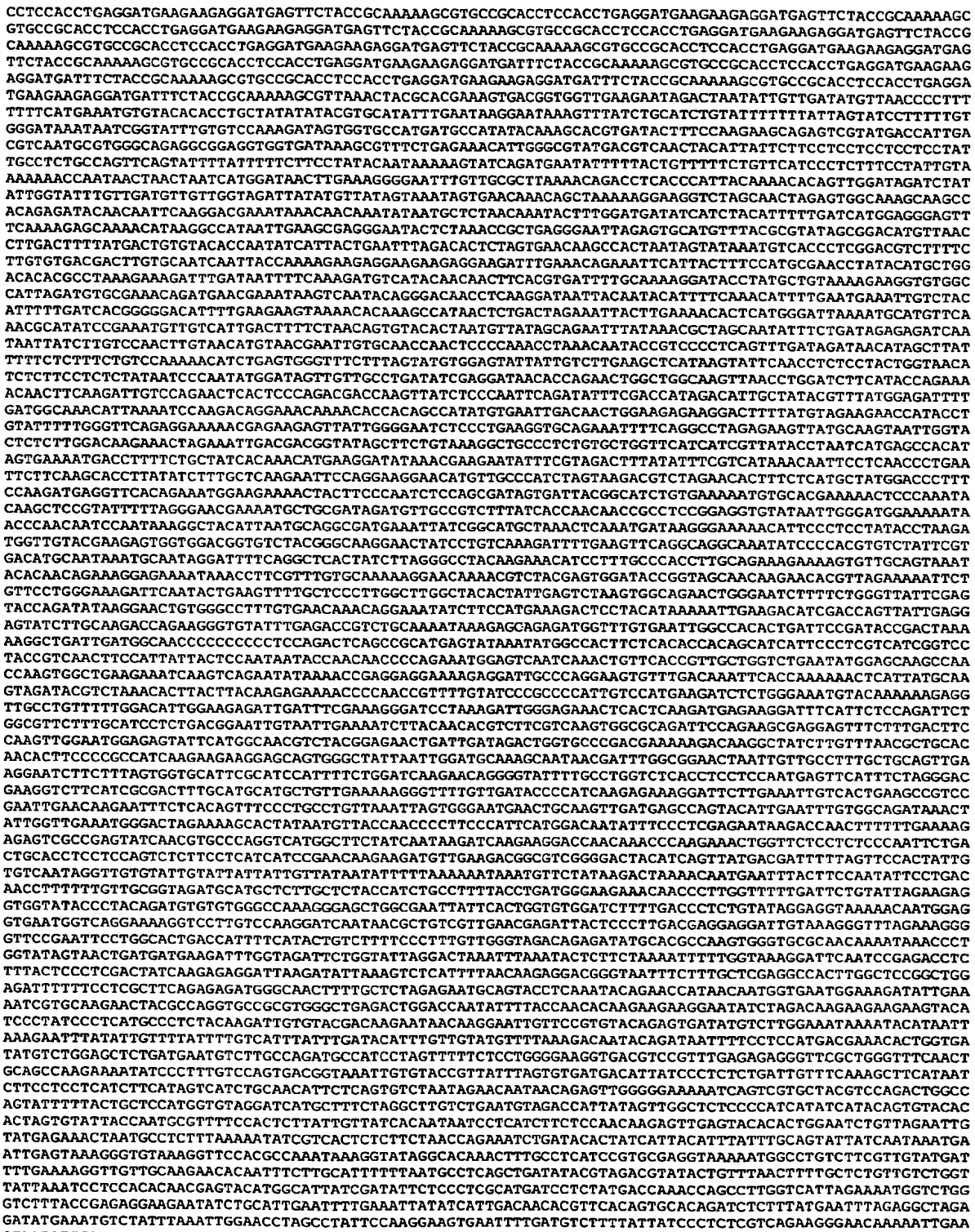


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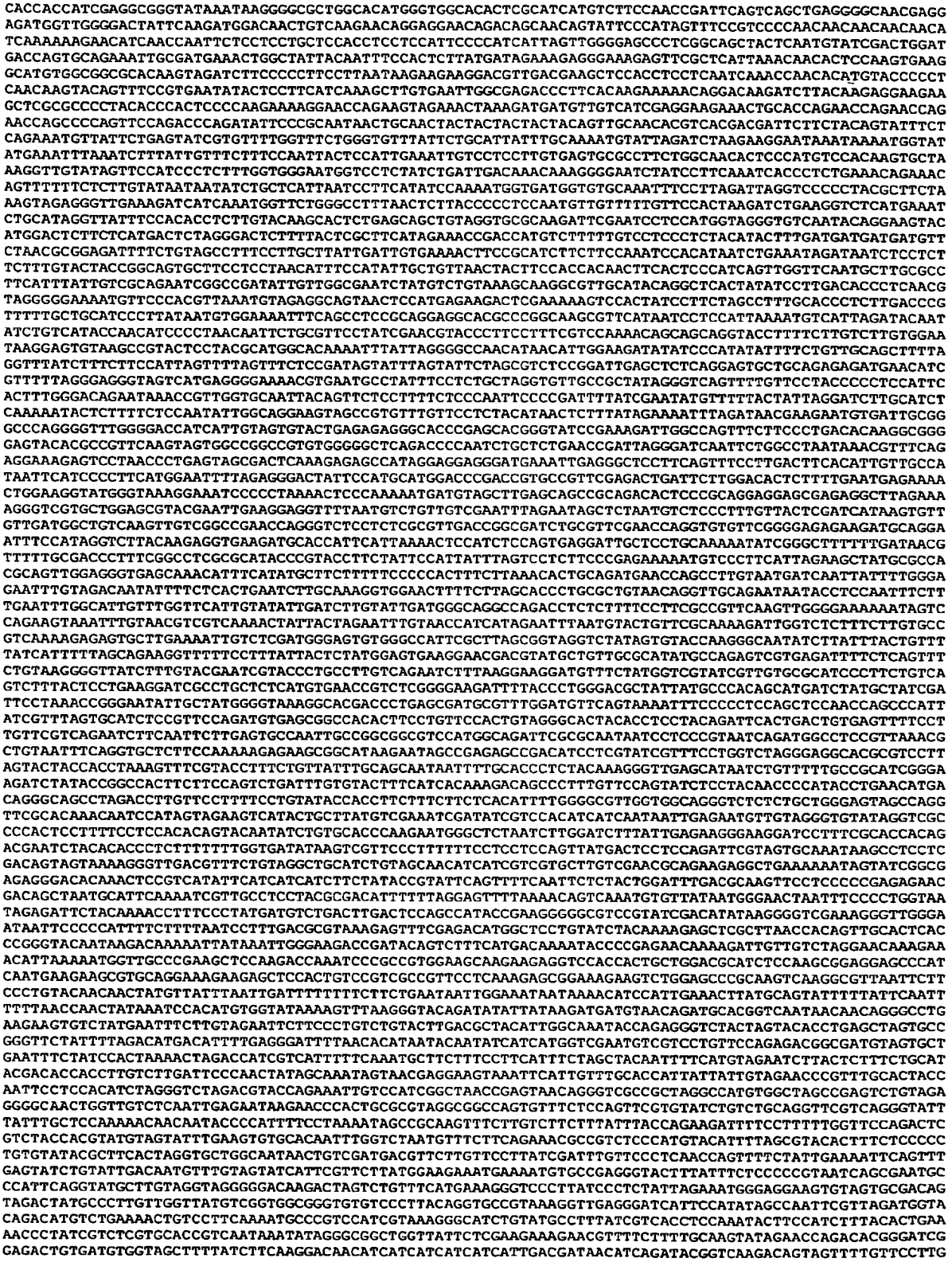


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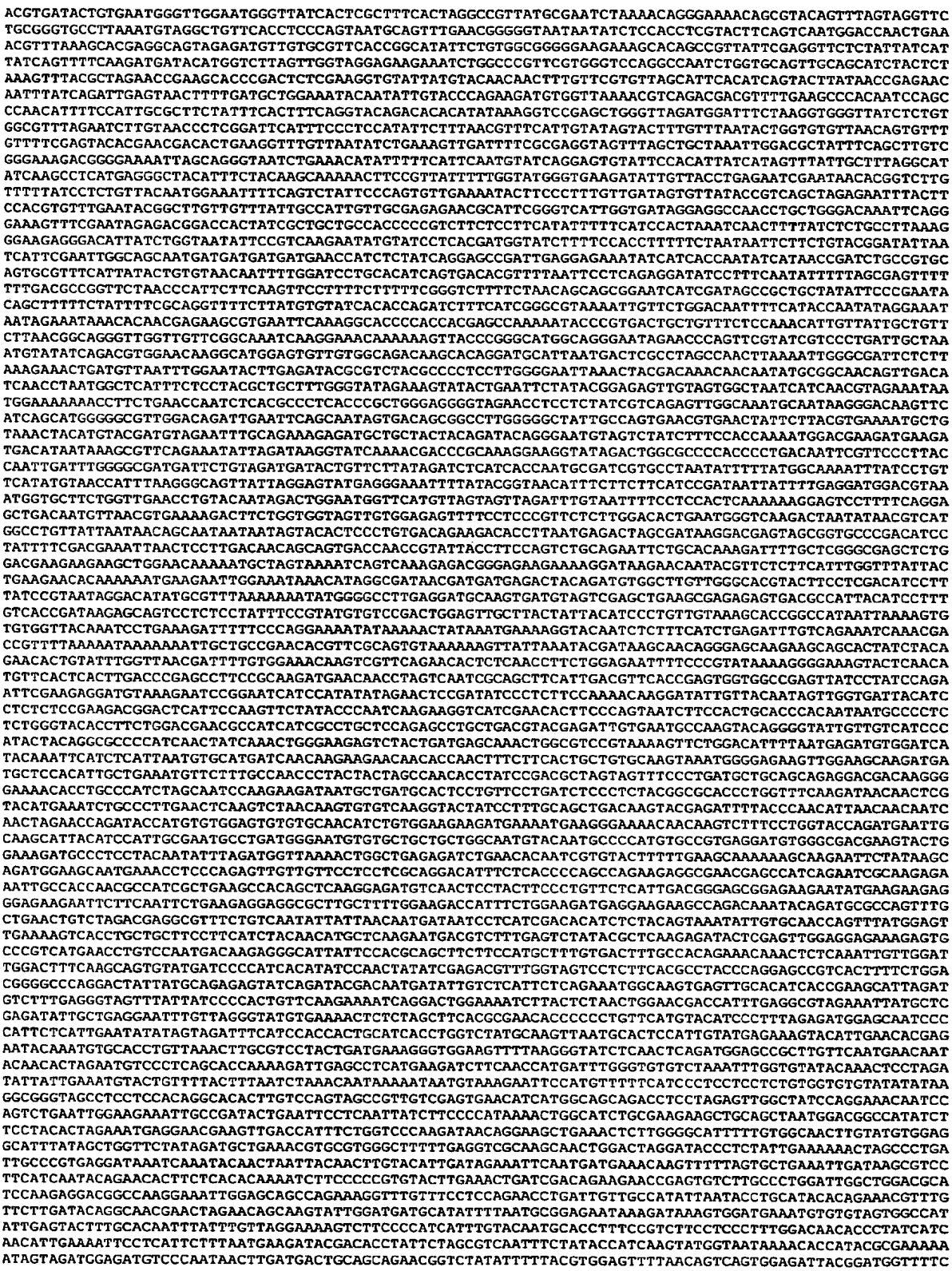


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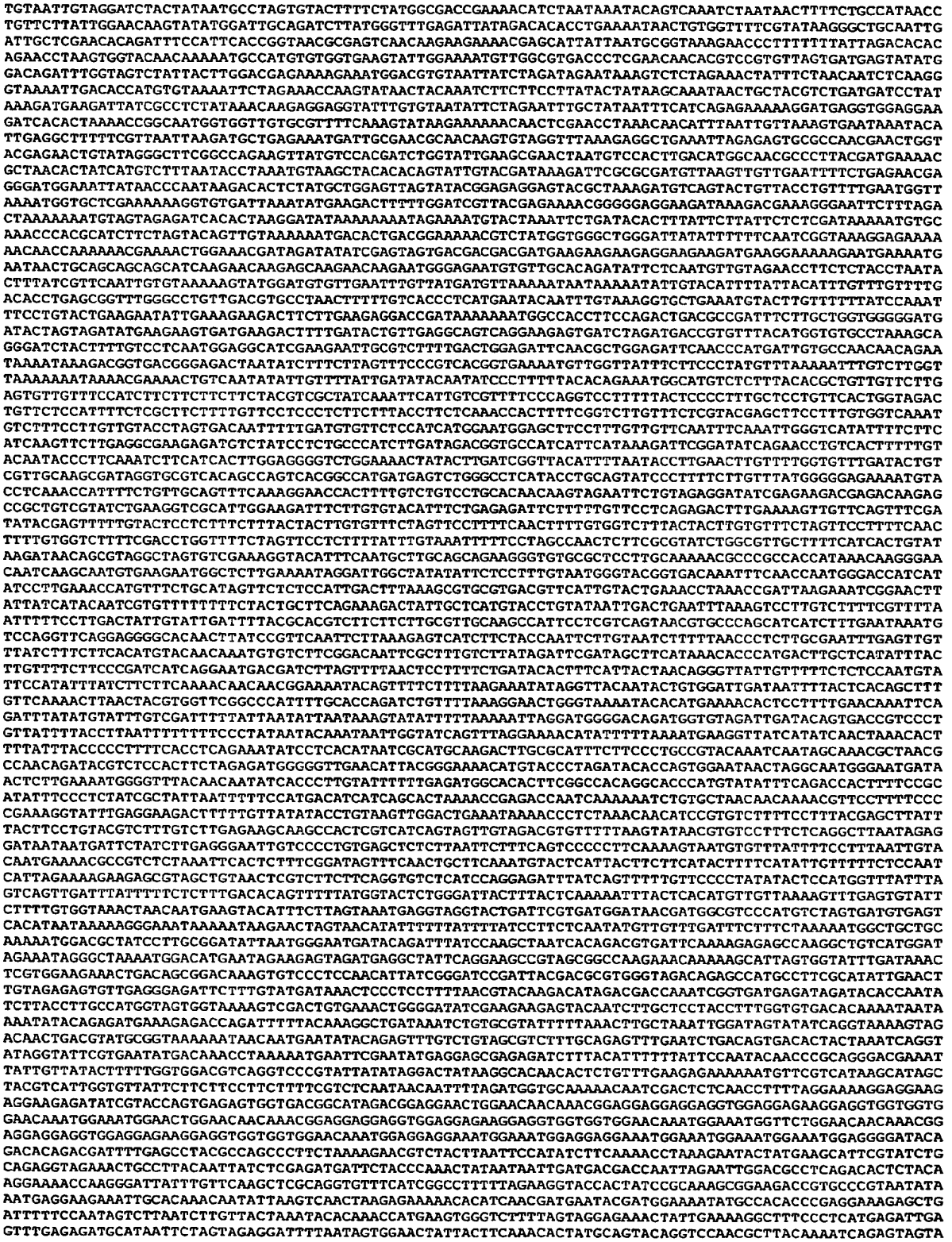


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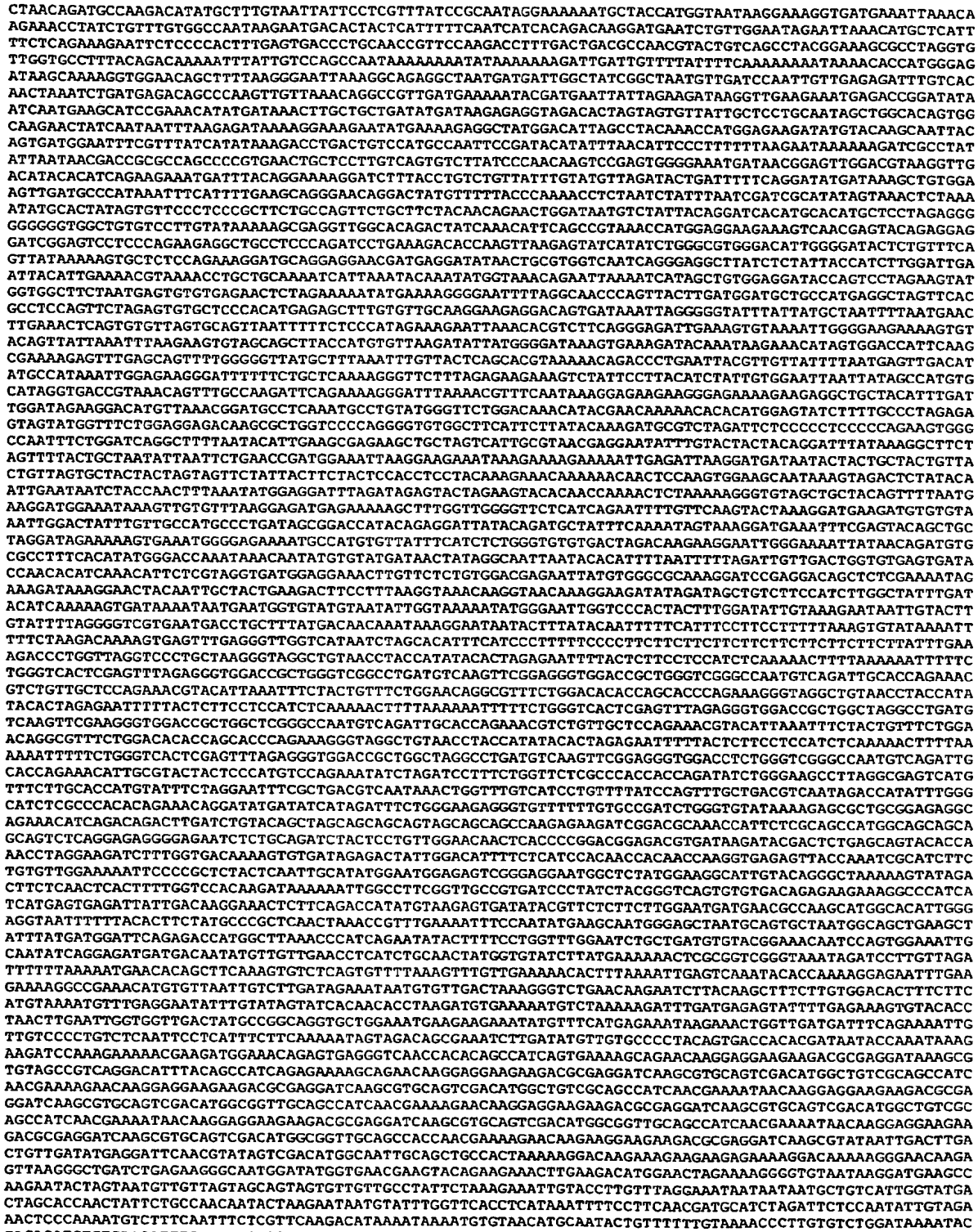


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CCCTCTTCCTTTTCCTCCTCTACATCACTGAGACCGATAGTTTTTCTAATAAGATTCTTGAACTTTCAATAGTTTCATTGTTGT
AATCGTAATCAACTTCCTCCTCGTTTTCATCTTCGTCTTCATCCTCACTGTCGCTGTATGCATATGCTGACTTTTCGTCATCCTCTTCTCCAAATACAGT
ATTGTTCAGTGACTTGAGGTTACTCTCCCTCTTGGCCAACCACTTGTCGTTCTTGAAGCAACAACATCCATTTCTCATAGATTCAGTGACACTTTCTTCC
ACAATTTGGTTAGTGGTCTTGAAATGTGTTCCTGCCTTCTTGGTAGACGAAGAACTGGGAGTTGACATGACCAATCCAGTTGACTTGATTGCACTATCAA
TATAGTTTCCTCCAAGTTCCTTAAACAGTGACTTATCTCCATTACTTCCAAATATCTGCCTCTTCTTCTCCAAATCCATCTCGTCCACATATACAGCATC
AGAGAGCTTCAATGTGAAGAGAGGGCCTCCCTTATCAAGGGCCTTCTTGTTGAGTGTTTCAATAGTCACGTGCTCATGGAACTGGAGATTCATACAACCA
AGGAATAGATTGGCCAGTTTTGTAGTATCAGTGGCGATTGCAGTTTTCTTCACAGCTTCTCCCTCAACCTTGACAATGTTGCTAACCAGATCCTTTCCTT
CAAATGCCGACTTGACCTTTGAGACACACCCATCACAAAAGGTGGAAGGGGACAGTTCTGTGCGTCCAGAGTTCATCACACTATTGAACAGTACCGATTT
CTGCGCCTTCTTATTCTTCTCCAATTCTTCGTCCTCATCTTCGTCATTCTCCAGAAATTCAGCAACAGATTTGGCCAGAACACTCACGTCAAGATGAGCT
GGCACCTTGCCCATAAGAGCGTCCAGTTCTTGAAGAGATTGCTGCTTCTTCTCGGCGGGTGTGATTTCTGGAGGAGTCTGCTGCTGCTGTTCTTCTTCCT
CTCCTACAACTTCTTCCACAGTTTCCGTGTGTGGACTCCTGATAGTGTTCCTCCTCTGCTTAGAGACCATTCTTCTTCCAGCAGCAAACTTGGCCTTGGA
AGGAGTTGGTTTCTTGGCAGAAGTAGTAGTAGTATCCTCAAATTCATAAACTTGATCTGGTTCCTCAGAGAAAGTGACAGTTGGCTGCTGCTGCTGCTGT
TCCTTGATTGACTCCATTTTTAGAATATTGGGTTATTAGGATTCAGTAGTTCTGTTATTCCTAGACAACACGTCTTGTCTGTACGATTAGTCGAGATGAT
GTGATGTAGAGCCCTTGCCCGTGCCTCAATATATACCCCTCAGTAGACCTTGATAATCACGGTTGCCAAACAACAACGGTTGGAAATCTTAGTAGAAAGA
ACCAATGGAACAAGTCAGGATAATAATATACAGTATAAGCTTTTGGGGAACAACATTCATTTATTGTCATAGCGCTAACATTAGAAGTACAAGAACAGGT
GATTCTGCATCCAGCTCATTTTGTTCAACCCACTTCATTTGCAGGGGACAACACTCTTCTTTCTTGAAAAATATGGATGAAGACACTTGGAATTCTTCAA
TAGGCCCTGGGGCGTTGCTGGAGGAGGACGCAGAAGAAGAAGAAGAACAGCTGCCGTTGAACGAGTTTATAGTTTCCAGAAGACAACATAATTTAGCTGT
AATTGGACGAGGAGACTTCTTGTAATGAGAGAACCACAAAATTCTTCTTCCCGTCTTTTCTGGTATAAAAGTAGTCCCATAATATGTTCCTTTCTGGACT
ACCACATTATCTTCGTTTAAGGGAACATATCTGACCGACTTTCTCATCAAGGGCTGATCTCCATTTCTTGTTGTGCTTAGAGCCGATTTGTATTCCCCGT

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CGTTCACGTTATAGTTGCATATAGAACAGTGGGATGAAAGGAACTTGTCGGTTACGTGTTCAGTTTGTACAAGATAACTGGACGCATTTGCTAGTTCTGG
AGGGACGTCCTGGTTTTTGTTTATTGTTGAAGTAGGTTTTATCTTTTTCCTATTTAAGCACACACCCTTTGAATTAATGTGTATGCGATTCGCATTGATG
TATATGCAGATTGTGAGTGCTGGAGAAAATGGTATCTCAAAATCGGTAGCTGGTTCAATAATTTCTGGTTCAACTTCCTGTTGTTCTTCTTCCTCATCTT
TCTCTTCCTTATTTTTGACACCTAGAACTCTAAGGTTGGCAGTACTAATTATTCTGGCTGCAGCCGTGCTGGTAGCAGAAGGGGAAGATTGTTGGGAGAT
AACAGGAGACATGTTGACCGTGCCGTGTCGTGAGGATAAATGGCTAAAGGTATATACGGCATGCCCTTTTTTCCGTTACTGTGTGCGAGGTCGTTTTCTA
GGACCGTAGATGACCATCTGCCTTCCCTCTCTTTTTCTGGACAACCTTTAATTGCCATGGTGTTATGAGAGGTAAACTCGCCTCATAGAATCCGCAAACTT
CCTCTAAAGGGAACAAGTGTTTCCCCATAGGGGACAATTCAAAAATATAATTCCAACATATTAAGGGTGTTGTTTTATTTTCCTTTTCATCGTACTCCGT
TATTGTTTTACTAAAATTTGGAAGGTGATTTTTTGATAGACTATCGGACATTATATCCGCTGCAAGTTGACGTTTATGTTCAATGACATAATCATTCGAA
TCAAAGTTGTCGTGTGTTGACACCATACCATTCCATTTCCATTTGGCTAGTTTGGAGAGGGATTTATTGTTGCGCAATTTTAGACGTGCAGAAACGTTTT
GCCATATTATTTTAGAAAGTACAGGCAAAACAACATCCCTCACGTCAATACTGTCCATTAATATATCAGTAGAATCATTGAACCTTATAACATCTCTCTG
TATATCTTCGTTTGATGGGGCCAATCGAACTAGAGGAACTAAATCCCCAGTTATGAGATCGGTGAAAATAAAGCTCTCGTCATCAACAATTTTTTTGGAG
CCTATGTACATCTCACACTTACTATAAAAGTCATTTTTATACCCTGGTTTCTTTTCCCACCTAGAACATAAGAGTATTAAAACTCTCGACAAATTATACA
TGGCACCTACTCTTCCTTCCATATTACTGATAGCTCTATACATATTAACCACGTATTGTATAGGTGCTTCTACGTACAAATCTGAAAATCCACTAGCGGC
AGTTCCTTCACTAAAGGCTAGAACTTGTTCCATAGTCTTCTCTTCTGAAAACATTTGCTGAATTATTTTAGTGGATAGTTTGTGCCGCTTATTGAATTTT
GTGCCAGGGTACTGGGACCCGAATTCGTTGAAATGTTGTTGTTGTTTTTCCCTACTTCTTTAGTTTCATGCCAGGCGGGGTGTTCTTGAAGAGCAGCCA
CCTCCAGGAACAAATCACAGATGGCTCGTACTCCATCACATGTGCATTTTACAGTTTCAGGGAAATTTAATCCTGTTATTTTATAAAACAACTCTCTGTC
TATTATTTTTCCCATTCGTAGGCGATTATTGACATTAAACCCACAACACTCGCCTCTGATTCCCATTATAAAGGCTAAAGAATATACTATAATATTTCCC
GCACTTGAACCCACGAGTCTAAGAGTTGTATATTCTCCATCGCAGTTATAGAGACATCTTGCCAATTCGTCCATTGATTTCCTGCCCGTGAAGCGCACAT
CCATGAGTCTTGCTCCTCCATATCCAATTTCAGCGTTTATTGAAGTCCTCCAACCTTTATCCTTGTTTAGGCGCTGTATCTTTTTCGCCTTCTCTGCCAA
TACATTCATAAAAGTGTAAAATTTAACGTCTCTTACAGATTCCATAATTTTTTCCTCAAGTGTTAGCGGCGGCGGTGGCGGCGATCCTTCTTTGTAGCCT
TCAAAGATAAAAGAGTGTTATTCAACTTACAGTGTTTATTGGCCCAGCAATTCTTTTCTTTCATCAACTGCATAGTAGAAGGTCGATCGGAAAGAATGAC
CAATTTGGAATCCAAATCCCTAGGTTTATCTAGTCCAGCTTCTATGTCCATACTCTTTCCTCCTATTATCATATAGTCTTCAAACAGTGTTTTATTAGCA
GACATGTTAATCATTTCAATTACAGTCTGGAGGCATGTTTCATGTCTATTGACCAGATCTTCATCATCTTCATCCCATGTCACACCCACCAGAATATTTT
CTCCTTTCTTGAGTTTGGATACATTTTCTGTAATCTTTTTCATTATCCGTTGTTTCTTGGACGCCACACTTTCGTAGCATAGCGTCGGTAGGGGAGAGTC
GCAATCCACAACCAAGTATTTTTTCATGATTAATTTGTTGAGGATTGTGTTCTTTGAATTGAAGAAAAAAATCATTCGTTCTGTACCATGGAGACAACTA
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CAATGATGCTCAAGGTGTATTCCGCCAGTTTGCAGATATCATCATTAATCTTCCCTCTTTTGATGATCTTAGAGACGAAGTAAAGGATGAACAAACTGAG
CTAAAGACCATATATGACTTGTATAGACAGGACATGGAAAAGGTGGTGGAAGAAGTTTTAGGGCGCCAAGACCTGTTTGATCACAAGTCAGAAATAGCCA
AAGGTTTGGCCCGTTTCGATACCCACGTCTCGTTGCTCCCTTCGGATAGGTCGGCTGTTCTAGACTCGTCCATATCCAAAGAGTTGGAAAAAAATAGCAA
GGGCCCGAACAGTAATATTTTTGACACACTAAACACACTCAAGGAAGAAATCAAAGAACTTTTATGTCATCATGTCAAATATTTATTGCAAAATCTTACA
CCGGAGGATGCAAATTTTGTGTTCAATAGTTCTGTAAAGTATGTAAAGAAATCATATCAATACTACATACAAACATCAGAGATGGAAAGTGATGAATTTA
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CCGACGGCTTTTTTAATGCAGCGTGCGTCCTAATTTCCCAGTGCCTAACGAATGCGAACCTATTATCTAACGACTTTCCTAAACCCATTGAACTGGCAGC
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ACTGATTCTAAAAACAGGAGGTTACTTCCACGACACGAGTGAACTCGGCAATAAAATTAGAAATTTAATAGACAAGGATGATTTGCGGGCGTAGCCCAA
TATGCAGTAACAATCACTGAGATGCAATCTACGCCAATGAATCAAAGATTAGTATCTAGTCTTTTAGATTTGATAATGAGACTAAAAGAACAAGTAAAAT
ATAGTGTTGATACTGAAAGTACTTCCTCCACCGCCAAATCTAATAATGCTTTAGATAGTGCTAAATTGACATCTCAACAAGTGGTTACAATGATGGTGGA
TTCTGGAGCTGAATTGGCAAGGCTAGCTGCCTTCTTTTTCGTGGTGGTGGATAATACTGTAGTTAATCGCCATGAAGCATTCATTCTAACATCAAAACTT
TTACCCTCGAATGAAAATAGAGGACTTAAAACTGTTGTAGAGTCATTCTTTAAAAATTTAACAATTAGTAACAAAGTCTCTACCTCGAATGAAGAAATGA
TGTCGGTGATGCCGTTCGAAGACGAACAACAACAACAACAATGCCCTCAACATGAACAACAACCGGATTTGAAAAGAGTGGTGGGAGAAGTATTTCTAGA
AATGGGAAAATCAATAGTGAACTCATTCCCTTCCAATAAGAGTGTACAATTAACGGCTGACGCGTTCAAGCAAAACTACTCGCCTATGGGAAGACGCATA
AATTTGGCGGCCAAGATAAAAACGGCTATATCTATCGGATCTAATATCTCGCCCAATATACTATTTTCTAACCTCCCAGAATCTGTAGGGAATAATACTG
TAACTGGTCTAAGGCTAACCAACCTATTGAAAAACATATCCCAAAGTGCCCAAGCTAATAATATAATCAAAAATGCCAACACGCTCGTAAACAATACGAT
GGACCAACAAAACTCAGCAGCCATGTCCATACTACTCTTTCCTCCAACATCAAAAGAAACTTCTATCTTTCCCGGAAACGATCCTTCATCTATAAAATTA
CAGGATATGACTACAATGTCAAATCTGGCACGAGGATTTTATTCCATCGCAGAAGGATGTATCGGGGTCGTACGCTCGAGGGAATTTGATGAAGGAGGAG
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TAATGCGAATATGAACCCTTCTAATGTATTAGAAGGAGGATCTTTTGTAGACGGTGCTCTTTCTTACATGTTTGAAAAAAATGGCAGTGACTGTGAACCC
ACCCCTCTAGCAAAATATACAATGAAAGATGTATCAAATCGATACTTGAAAAAATTCAACAATGATAAAAATACACAAGATTTATATAAAAATAGAGCAG
AAAGAGCACTCGTCGAACAGGTTACAAATAAGCCTACAAGTGTTGTGCATTCCCAGCTAGCAAACGCCATGGGGGTAGCTGTTATAGGCGCAGCATCAAT
CAAGCTCATGGAAGCAGAAGCAGCGGAATCTGAAATGAGAGCAGCAAATTATCAAGCAACATCAAAATCTACAAATGCTATTAATATAACAAATACAATT
GGAATGATACGTAATACTACTCACCTGTGTACGACCATCGCCGTGAGTGCAGCCGCCGACATGTCAAAGCTCGCCAACAACCATTTTATGAGTGTATTAA
ACACTGCAAATAACAGTCATAGCAGCAGACGAGGAGACAGATCGTCCCTGATGTTGCAGCAACAACAACCAACACATTCAGCATTTCTGGAACAGACAAG
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GACAAAAATACTACTACTACTACACCCAGTAATGCCGGCCGGACATTAGGATATGGATCTAATATAACTGGCATAAACACGATAAAACAAGACGACAAGA
GTATGATGGATAAACTTTCTGAGATGTCTAGCTTCAGAACTTAAAGTGCCAATTTTCATATAAAAATGTAGTATTATGTGGTCGTTTTTAAACTTTAAGC
GTTTGTGGTTTTGGGTCGTTCACGGTCCAAGATGTAAGAGTCCCCTTGTACCCAAATTATAACAAAGTGTCAGTATGGTCAATGGAAAGTATCTAAAAAT
CCACCCGTCTATCATTCAATATCCCAACTGAACCAACCAACCCCAGAACCAACAACATGTCTCTTGTTGAGAATAATACCCAAGAAGAAATGATTCTGGA
AACTACTGTTGAAGGTGTTGTGGAGGGAGCAGAAGTTGCCCCTAGAGGTGTCAAGAGACCCCTTCCTTCTTCCTCATCTTCTTCTTCAGCTTCGGATAGT
GAAGATGATGAAGGAGGAGAGCAACCACAAACGAAACCCCCAAAGAAGAAACGTAATATCAATAGCGGAAAGTACTGGAAAATCGAAACAATCGAACCAG
CATCTCCAGAAATGCTCAGTGCTGTAAATGATATTGATAACGTGTCCAAAACTATTCCTCTAATCGATAATAGTTTTGGCGTTCAGTTTAAAAAGAGTGT
ATCTGAAGAACAGATCAAAACGCTACTCACTGAAACTATTGCCGTGGAATATGGAACAATCACAAATGTTAAATATTCAACCTTTAATCAACTCGAAAGG
ACCGGAGAGCCTCTTAAGAAGAAGCGCTCAAACAATGGAAATAACAACTACAGATACTGGCAAATTCGAATTGAAGCCGCTGCAGCAGAGAATGTTACAC
AAGCTGTTTTGGACGCAATCGTTGAAGGAAATGACACCGTGATCAAGGCAATCCTCCTCCCTGAAGGGGAGGGAATCGGGCTTCAATTTAACAAGAGTGT
TAGCTCTCAACAAGCTAAAAATATTGTCCAGGCTGCCGATATTGAATTTGGACAAGTTGCGCACATGAAGTGTAATTTGTTCCACAAGATGGAGAAGGCC
GATGAATCTTCTAATTCTTCTGGTGAATCACCAAAGGTTAAGAAAGTAAGGAGGAACAAGTCCCAGCCTACAAATTCTTACTACACTTTCACTATGATCG
GGGATTCTCTTCAAGAGCGTATTGATAACGCAATCAAAGTTATCGAAATGTCTCCAGTTAAGAGGCCATTCTCCAATTCTGCTGCTGCTGCTGAAGAAGA
CACCACTACTACGACCACTACTTCCACTGGTGTTGTTAATCCACGAGGGATTAAGGATATTCACTTTTTCGATTCATCCATTTCTAAGGGATGTTTCACT
GTGAGGAATATTGTTGCAGCAAATGGTGAAGTTCCACAAGAAGAATTCGTTTCTGAGTTGTACACTAACCTTCTAAAGGTTGAAGAGAAGGTGGATCATC
CTACTTTCAAGAAGCTTATTCATGACCGTACAATGAATCGACACATTAAGGCATGGTACTGCATCTGCCCCTACTACACCACAGGAGGCGTCCCCCCTGC
AGCTGATAAGGTTTCCGCTAAGGGAATTGCTACCTACAGAATATACGAGGACAGGACTGGAGTGTTCCAATTCGATGGGGCACATACATCTACTACCCCA
GCACAGGCAGCCGAGGCAACTGGTGCTATTCACAAGTCTATGCTCTTCCAGAGTCCTGGAACTGATATTCAAAAGTTCCTCGATGCTAAGAAGGCAGAAG

FIGURE 2, Sheet 20 of 40

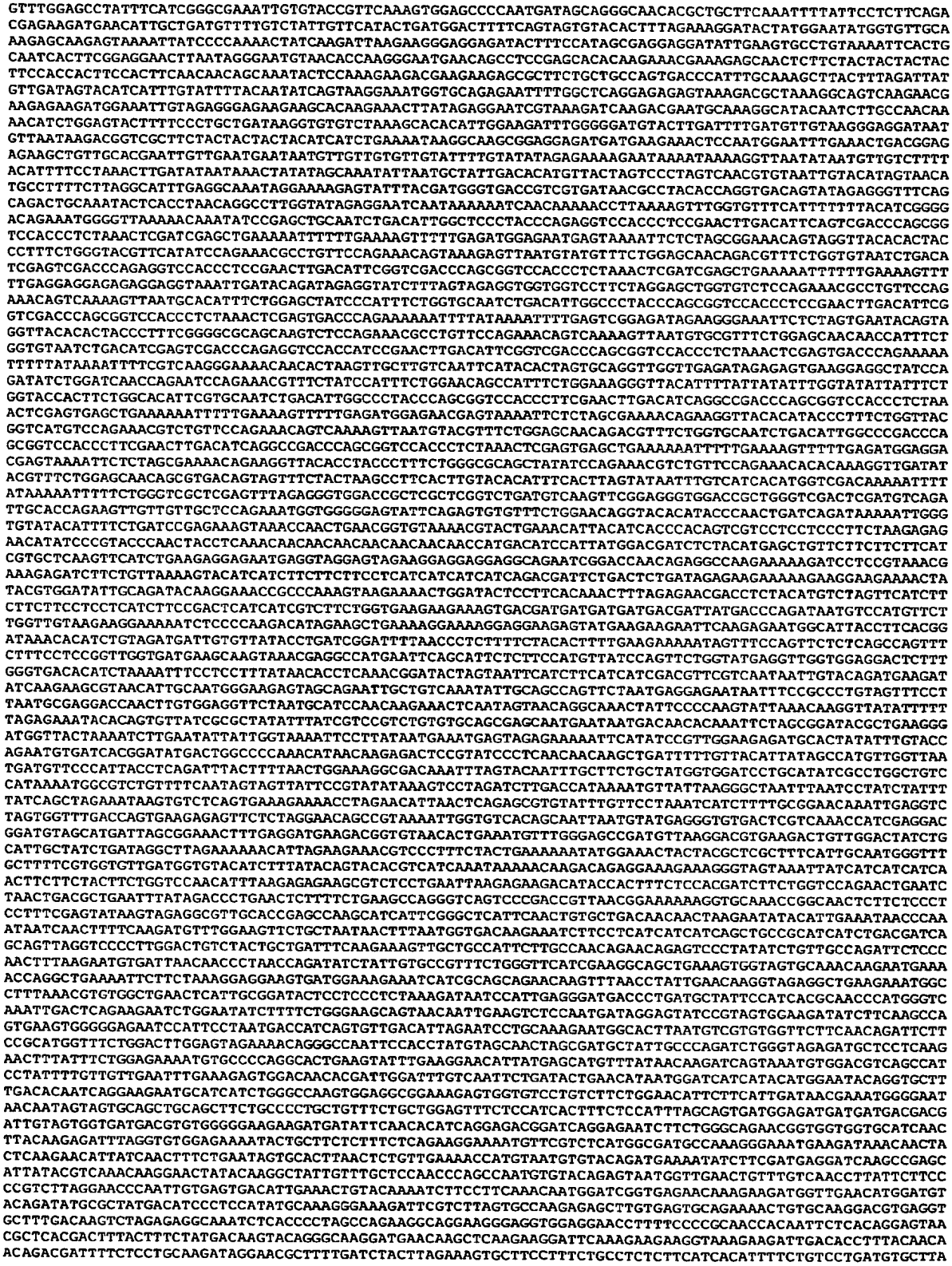


FIGURE 2, Sheet 21 of 40

TGGTGCATAGAGGAGACAGCTTCAATATTAACTTTGCAAACAACAAACTCGAGTGCTATAATGAACGTAACGGAATTGAAGAAGTTACTTCCTCACAAAC
GGTCAACGCCAAGGAAGCACTTGAGGATATTACAAAAATTAAAATGAAGAGAGGGGATGATATTATAGATGTTGTGAAGAGTAAAGGACTTTCTTTGAGG
GAATTCTCTAAGAAGGTTAGTAAGATTGTGAGAAGGTTTAATGAGATCACAAACCAACTCTGCAACAACTGCAACGTTAACTCTTCTAATGGAGATGTGG
ATTTCCACGTCTTTACTTCTGTGTGTGTCTACATCCACAACATTATTCCTGTGCTCGAAGATATCTCCATTTTTGCAGAATTGGGTGAAGAATTGACCAA
GCTTGTTAAGGAGTGTAGAGACGTGGCTGGAGAGGACAAGACATATGATGATATTATCCGCAATTACGAAATTACTGTAAAGTACTTTAAGCTCTTTAAT
GCACTCGTTAAATTCTGTCACAGGAATTATAATGTGGCAGTAACCTCTGCCATTAACAGGAGAGGGTACATGTGCATGGTGAGCAACCTTGTCGGGTATT
ATTGTAAGCTGTCTGATAACGCTATCCAGTATCACGAATCACTATGCTCTTTGCACTCTAGCATCTCTTATGCAGACTATTATACGTCTCGCAATAACAA
TTCTGAAGATGGAGGAGGAAACTCTTCTTCAGAAAAGAGCAATGCAGATGTAGCCAAGACTATGGCCTCTTTCTATGACCAGTTCGATAAGAGTGAAGAC
AGCAAGAAAAATAAGAACAAAACTTCAAATGAGATCCTTATAAAAATGTTCCAAATGGATAGGGTTTTGGATGGCATGGATGATGATGATGATGAAGATA
GTGATAGTAGTAGCAGTGAGAATGAAGAGGAGGAGGAAGAGGAGGAAATTGTAAAGAAACCAGCAAAGAAGAGGAAAGTGGAAGATGTTGATAGCAATAA
GAAGACACTGCCAAAGGAACCTGCCGTTAAGAAGGTGAAGCAGGAAGAAGATGTGGAGATGGAGGAAGTGAAGGAAGCAGCAGCAGAAGAAGAAAAGAAA
GAGGAACAGGAGGCGAAGGAGGAAGACGCTACTGAGTATGACGACGATACAGAAGAGGACGAGAAAGCAGTAGCATCTGATGAAGATGAAGATGATGAAG
ATTCTAAAGCTATTTTCTAAATATCATGTGTATAAAATGTAGTATTTTAAAGGTATAAATAAACACAATATAAAGTTAAACATTGTTTTTTATTTGACAC
ATGTACATCATCAATTTCACATGGTTATATTTCTTGTAGCTTGCTCGGCAGCAATAAGAGCAAGAGAAGAGTCATATAAAACAGATGTCTGTGAAGCAGC
CATGATACCCCTCGATATATTATTAATAAGGGGAGTTGCTGCTATATTAACAGCATAATAAATCAGGTTCTTCCAATCCCTAGAAGCCCACACATTGGGC
ATTTTTATATAAAAATCAACGTCTACTATTGACCTGGCAACAGCCACTATACCTAGCTCATCAATGTTAACAATCTTCCCCTGAACACCCATTACAATTT
TTGATTTTTCTGAATTCTCTCGTATAGCAGCAATACGGCTAGCTTCATTATTTAACCATTCCAATTTTACACTTGAAACATAAGCTGGGGATTTTTCATC
AGTTACTTGAGATACAATATTATTCCATTGAGATAAAAGTTCCTCCAATTGAGTTGTAGTCTTGTCCGCTTGCTCTTGGAAACTTTGCATGACGATAGCC
GAATCTCTTGTTGCAGTTTCGATGATGGAAATACAGTTGAGCCATTGCATGTCAGTAAGGATATGGCGCCGGATTAACTGGAACAAACAGATTCTGTGCAG
GAGAAAAGTTCAAGTCTTCTGGAATCTTGTTGAGGTTGATATTGTCCTTGGTGTGTTTCCATGGGATAGGTTTCTGTGCCTTTGAAGCAATAAAGTATGA
TGGGATTCTACTGTATTTCTTTAGTGTTTCTGAAATGTTTGTCTTTATACGGTCCTTTCTTCCATCATCCCTAATGTAATTCAAAAGTTTAGATGTGAAT
AGAGAAGAGTCTCTAATTTTTTGCATTTGTTCATTGTGAACCTTTATATCCTCGGGAACAGTATTGTTATTATTAGCCTGCCTCTGTTGACGCTGCTGCT
GTTGTTGTTGTTGAGTAGTACTTCCAATGGTATTTAATTTGTCCAATATTGAACGTAATTCTACAGGCACCCTTCTACCAGTTCCAAGAGCACCTCCACC
GCCGATGGCCGCTGCAGCTTCTTCACTAGCTTCATCATTTATAAAAAGTCTCCCCGAAGAAGCATAGCGTAAAGATCCATACCCTTCATTTCCAGTATCA
ATAGTAATCCCATTTTGTTCAGCTGTTATCCTTTCCAGTATTTCTTCAATGGCCTTTCTAGGATCTAGTGCAACATATAATCCATCGACCATAATATGAG
ACACGTGCTCGCACACTTCTTTAATAATTTTCATCTCTTCGTTGCTGACAAGCATCATCATTCTAGATATAATAGTAGCAATAACATTCCTAAATTTGTT
CTGAAGAAATAGTTCGATCTCTGTGAACGTAGGCTCGAAACGGGCAGGCACATTAACTGGAACAACCGCTTGTGTTTCTTGTTGTTGCTGCTGTTGTTGT
TGTTGGATCGCTCTTCTTGTTCCACCACCTACTATATTATTACTGCCTCTGAGTTGGTCGGCTGCAATAGCAATGATTTTGTACACCTTTACCAGATT
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AAGAACTTTCCAAATAAATTCGAATCCAGTTCCTGCCACTGTGCCCACTTTACTGGGGAAAATATCGATCCTCCCTGTAGATAGAGGACTAACACATTCC
TTATAGATCCTCATTGGGCTTAAATGTTGTGTCGATTTAGTTTTTGAGGCTTCATAAAGCACAGCAGACGAGAGAAGGGGTTCAAAGAATACAGTTTCCA
TGCCCAATTCCTTTACCGAATATTTGACTTGTTTAGATGCATGAACAGGAAGATTTGTGGGCTGAGAAGTCGTACCAGGGAGGAATGCGCTAACATGTTC
AATTTTCCCATCAACCGAAAAACTTGTCCGTACACCATCAACGAATGAAGAAGAAGAAGAAAGGGATCCAGTGTCGTCTTGATGGTTATTAATATCA
CCAATTTCCATATCCTTTATACCATCATCGCGTTCAGTATTCTTTACAACTTTAAAGTACGACACCAATTCACCTTTATTTTTCAATCCAAGGAATCCAT
CTTCTGCGATATTCTGACCATATGTCACATTTCTTGTTAGAGATTTAGGTGGTACATAATTTAAGAACGATTTTGAAATGGTTTCAGAAGAAAATGGAGC
AGTGGCAGTTGTTTGCTGCTGTTGTTGTTTTTGTTCCTTAGAGGATATTAGAGGTACATTAATGAAAAGTTCCAGATCCTTATTCATCTTTAAAAACCGT
CCTGTTGGTACAGGAAGATTAACTACCCTAATAGGGGTTTCTGATGAATATCTGGAGGAGGATGATGGAGAAGAAGCGACTGAAGTGGCAGACTTTAAGT
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AGGGAAAGCAAGGCACACGCCTCCATTATCGGCTGCCGAATGAATAACTGCATAATGTGTAACAATCTTTGCAATTAGATCCATCACGGGCTTCTTGAAT
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CCGATTTCAAAACGCAATCAAAAAATGGAAGAAGAACAACTTGAAGTACCTGCTGGTGCATGTACATCCAAGCGGTCTCATCCACTTTCACTGGCTGTCC
TCTCATAATATTTCTTGTCATTGTTTCTAAACACGACCGATAAAGACCCACCACGCAGTTAATGGGATCGTACCATCTGTACTGCCGTCCATAACTTCTT
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CCGAATGTAAGAAACCTTCCAGAATCGTGTATTTCCGACACGTTACTTTTCTGTCGACAACGAGTGTTTTATTATGTTCAGCGTCGTTAAGAGAGGTTA
AAAAAAGGTGCATTTCTATCCAGTCTGTTTTCTCCGATATACAGTCCATGATTGAAGTGTATTGAGGCCCAAAGAAGCAAGTAACTGGGTTTTTCATGGA
AATGGAAGTAGGTGCCCCTGAAGGGACAATGTTGGTATCGGTAGAAGTTTTTTGCCTCTTTGTACGTTTTCTATTTTCATCGTATTCCTTAGAAAGGGTG
GAAGATACATCTCCTAAAGATTTTCCTTTAGACGATAAAATCGATTGTGCGATTTTTTCCTTTTGTTCGGTCGTCAATGAGGCGGTTGAGGAGGAGGAGG
AGGCTGCTGTTGCTGTTGCTGTTGGTTCATAAAGTTTGGGTTGAGGTTTATTTTTAAATGATAGTTGATAATACCGTGTAACCAAATCCTTTAAAGAATT
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AGATGGGATATATTGACAAGTTCTTCCATGCCGTCGTTTCCTTTAAGATCTAGCCGTATTTCTTTCTCATCATGCATTGTCCAGTCCTTAATATTAATGA
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ACGAGAATAACATCCTCCTCCTCCTCGAGGAAATTTTTGTTCTGTCAGAGATGAAAATCGTCGTGCTTCTCGTGCTCTTTTTCCACTAATGCATTTAGA
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TTCCTAAACGCCCCTCGGTGAGGTTTGCAAGGGTAGAATCATAACACGCAAAAGTTCCCGCATTAACAAGCGGTAGAGAAATTTCGCTATCGCCATCTTG
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CAACCCCTATTATCTGTGAAAAAAACCCCTTCGTGTTTAACATGCAGAAGTGCTCAGACTGTGCTCCTTTCCCTCCCTACCCCGGCACTGAGAAGCCTTT
CCCTCCATACCCTGGTACTGCAGTAGAAGAGGAGGAGAAGCAAAAGGAAATTGAGGAGCTTCTGGTTGACCAATCTTTCCCTCCCCCATTCCCTGGAAAT
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TCATCGATCTGGAGAAAACCCCACCCCGTAGTGACGTTAGGCACGGTTACCACTACTTAATCAACCCCAACAAGGTTGGGGAGCTTAACCATATCGTTGG
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CGAGCTGGCCTGTGCAAGTTCTCAAAAAACTAGACGGTAAAGGTATGACCAAACCGGTATAACCAACTTTTTATATAAGCCTAATATTATAAATCAACAA
CTAACAAACGCGAAAACTAACAATAGGAACCATGGCCTCATCATCATCATCCCCTGTTGCCCTCCTCTGTCGCATCATCCGTGATGATGGAAAGAGAT
GAAGAAAATACACTGTCCCTCAGGAACAGGAATGTGAACAAACCAACACCTGTTAGCGCCGCCTGGGTGCCTGTTGATGAAGAGGATGAAGATAGGGAGG
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CTTACAAGCGCAGCCGTTGCTGCTATTTTTAAGACTAGAGATGTGGCTAAAACTGAAGAAGGCGCAGCAACCATGGAAGAAAATTCAACAGATGTGATTA
CTGGAGGAGATGGAGATAGTGGTATTGCTGCTGATGTTGTCTCTCTCGCTAGTGAGGGAGAGGAGAAAATGGATCTCTTTTGGAATCTATTGCAACAAC
ACTCATCAAGACTACAATTGAAAATCTTGTAGATGGTGGAGAAGAAACCACAGAATTGTAAAATGTTTTTTGGTATACAAATAAAAGAATACATAATTTA
TATAATATTTTATTGTTTCCTCTTAAATGACAATTTCCTTATGATACTTTTAGGTGAAGGAATAAAGGTAGGAGAAGGTGTGGAAGACACAATTGTAGTG

FIGURE 2, Sheet 22 of 40

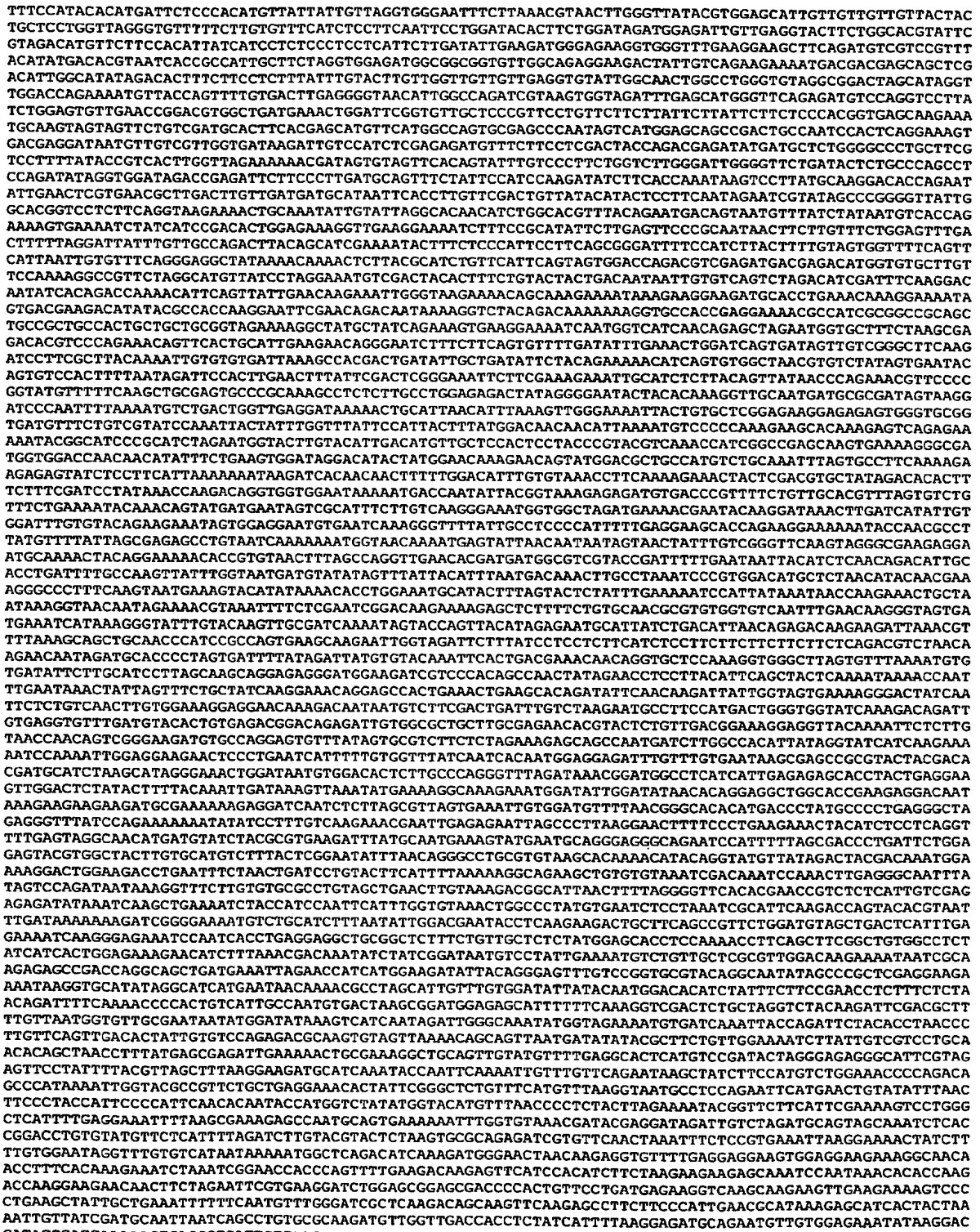


FIGURE 2, Sheet 23 of 40

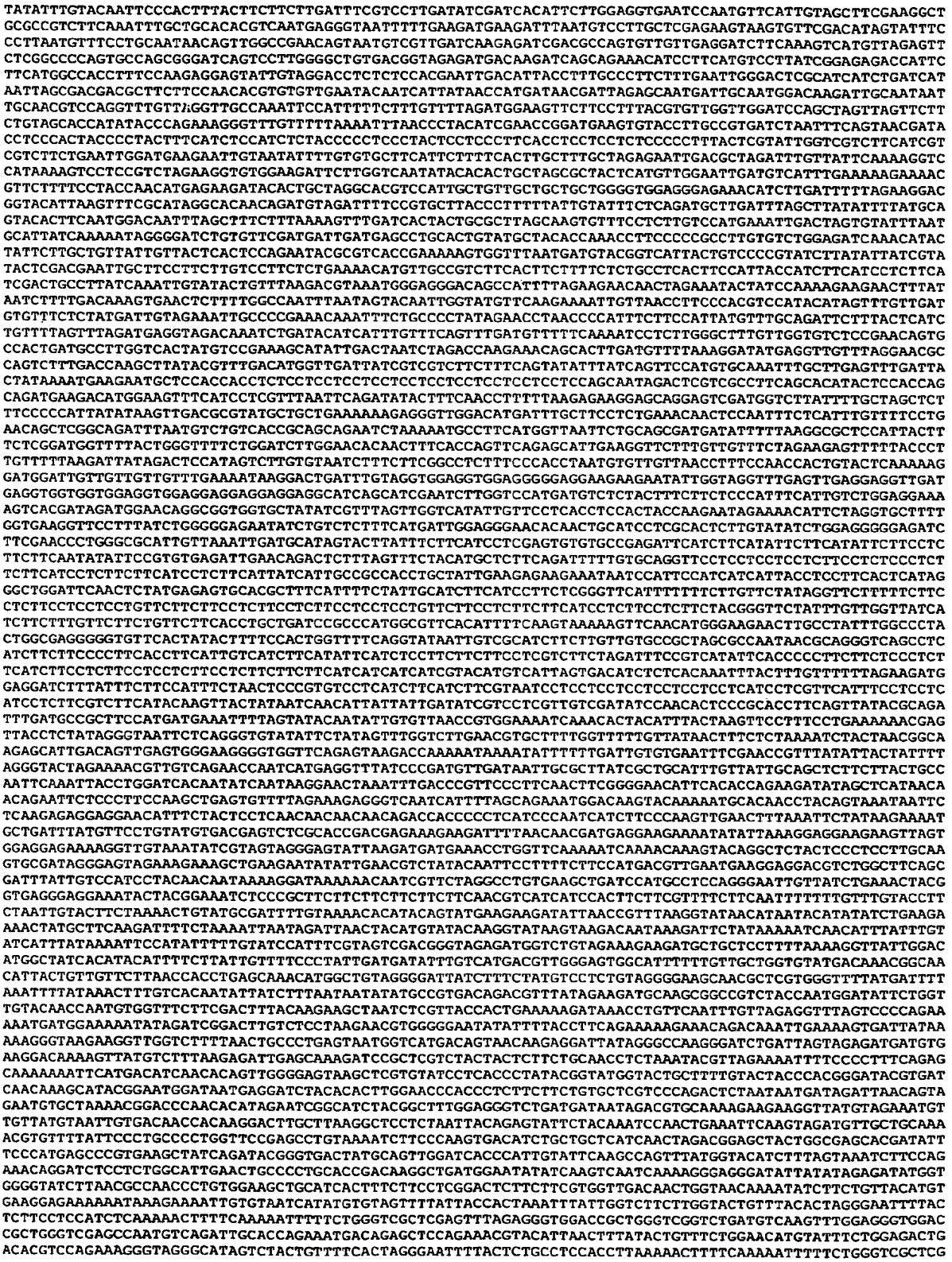


FIGURE 2, Sheet 24 of 40

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FIGURE 2, Sheet 25 of 40

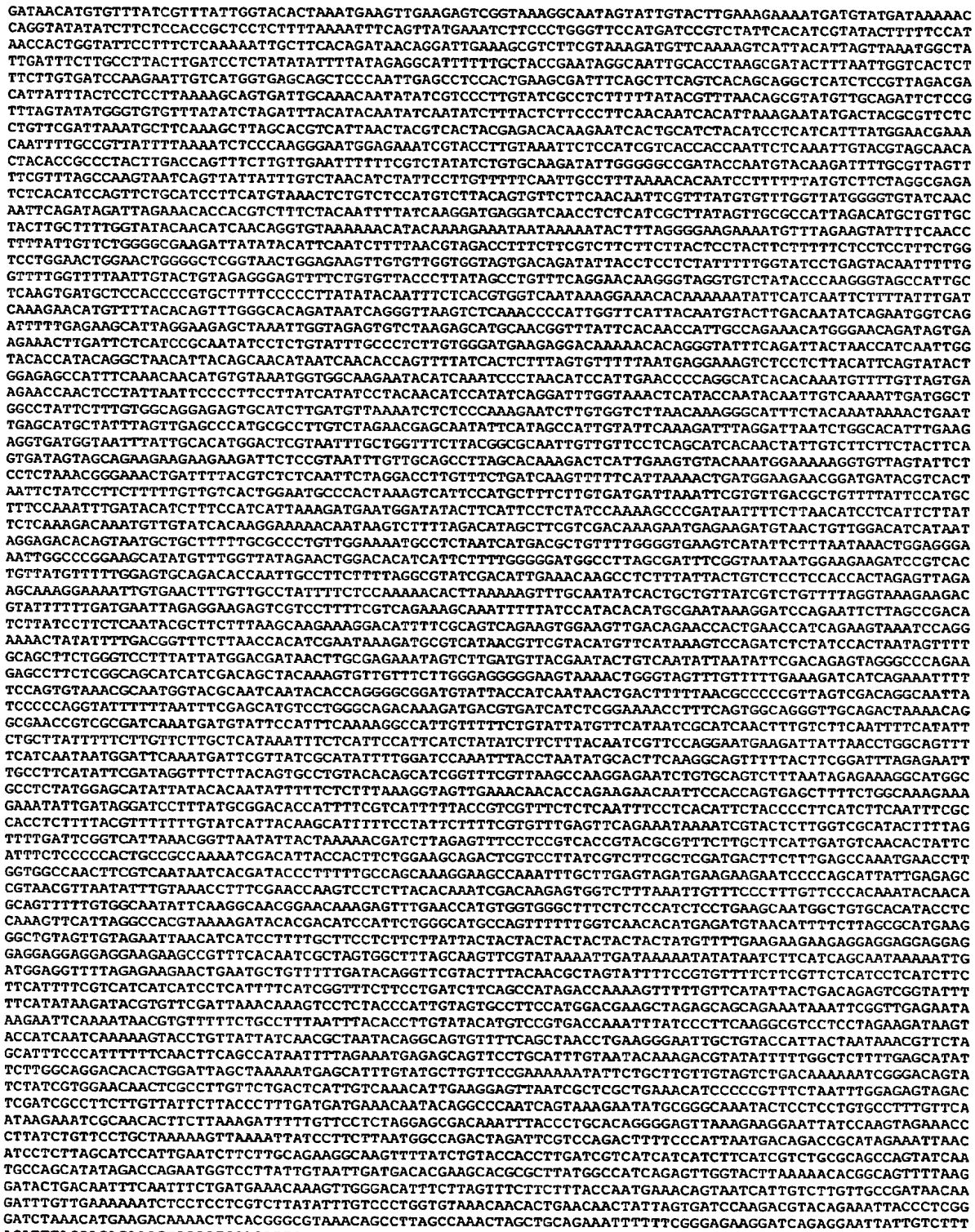


FIGURE 2, Sheet 26 of 40

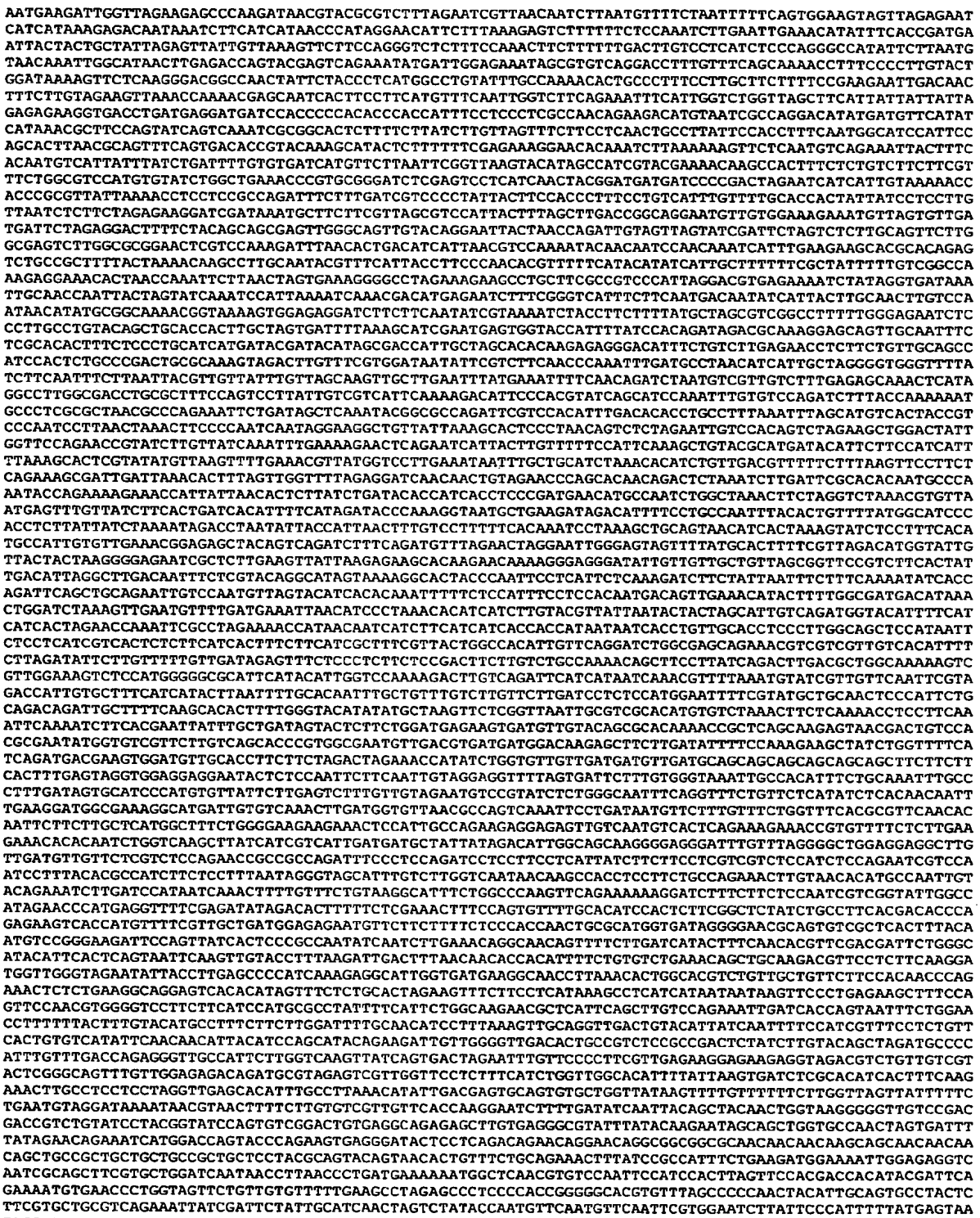


FIGURE 2, Sheet 27 of 40

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ACAGCGCTTTCACCAACCTCGTCGGATCGGAACATTCTCAGCGTCTAAAAGTAAAGAGTACTCTTTTAGATTCTATTTTCAACACTAGGATGGCTCACAC
TGAAGCAGTCATGGGTCTCGTATACCCTACAGCGTTCATCAACCATGAAATGCCCTCTGATTACACACAGCGCAGAGAGATGCAATCACTCGCTCTTAAC
ATTCTTAGGGGAGTTAATTGTAGCCAATTGCCACGAAAGGATATTGGAGACACTGCTGGCCTGTTGACCTTTATTACATCACGTAAATTTGCAGGTTATG
GAGGAGAAAGGGGAGGTTTGTCTCTATACAGAATGTCCATTGTTGATGCTCTTTCTTGCCCCTCTGACAATCGGCTCAAGGGAGCAGTCTCTCTAGAGGT
AGGAAAGTGGCAGGATATGGGAGAGGAAATCTTCTACAAGAGGAGCAACGATCTGGTCGATTTTTGTTCAAAGAACAATATTTCTCTGGAAAATGCCGTA
GGTCCTATTGCTAGGTTTGTTCCCAATGGAACTAACATGGCTGATATTGGCATGACCGATATCATTTCTAGAACAGTCAAGGATGACGCTTCAATGATCA

FIGURE 2, Sheet 28 of 40

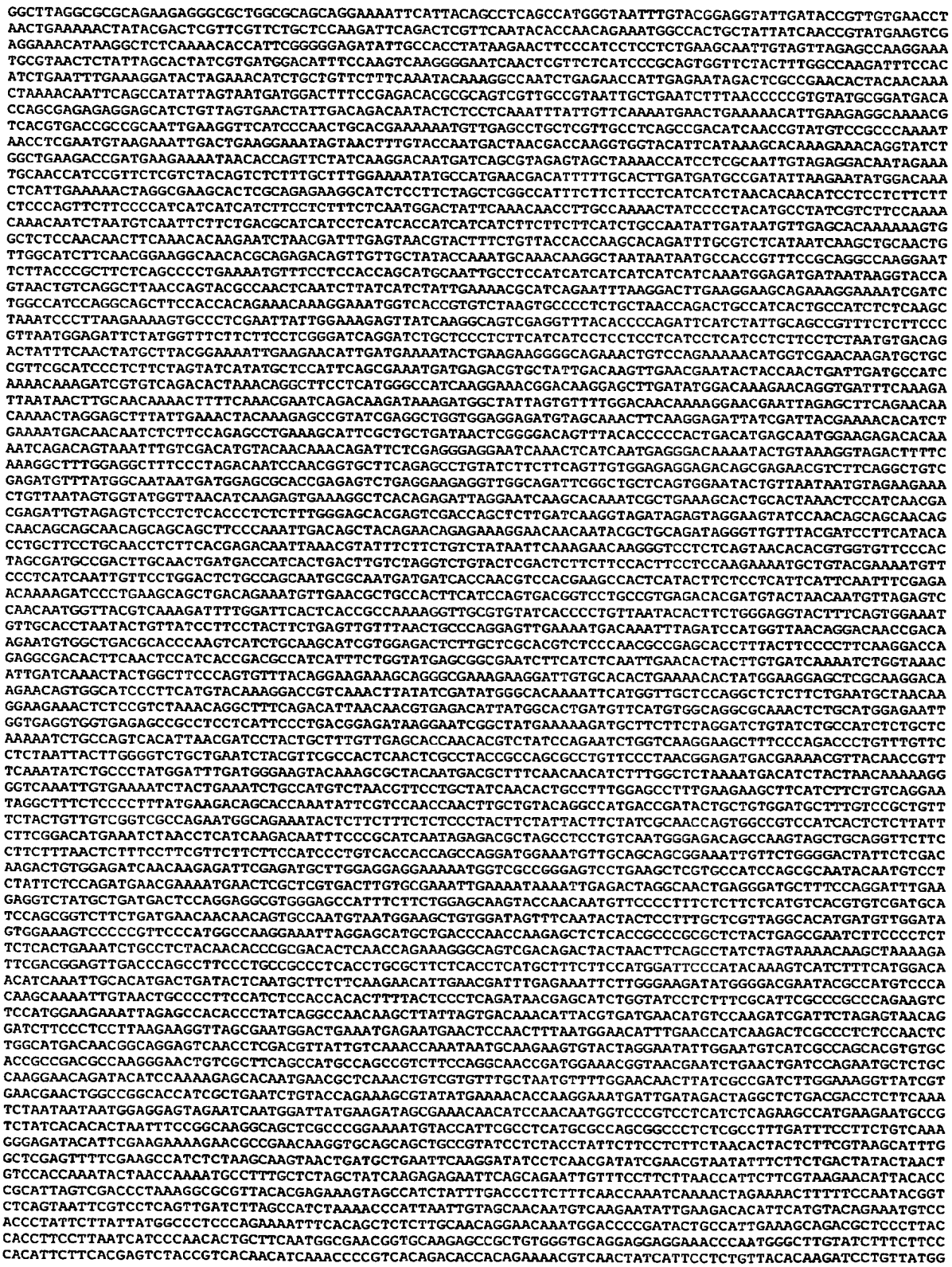


FIGURE 2, Sheet 29 of 40

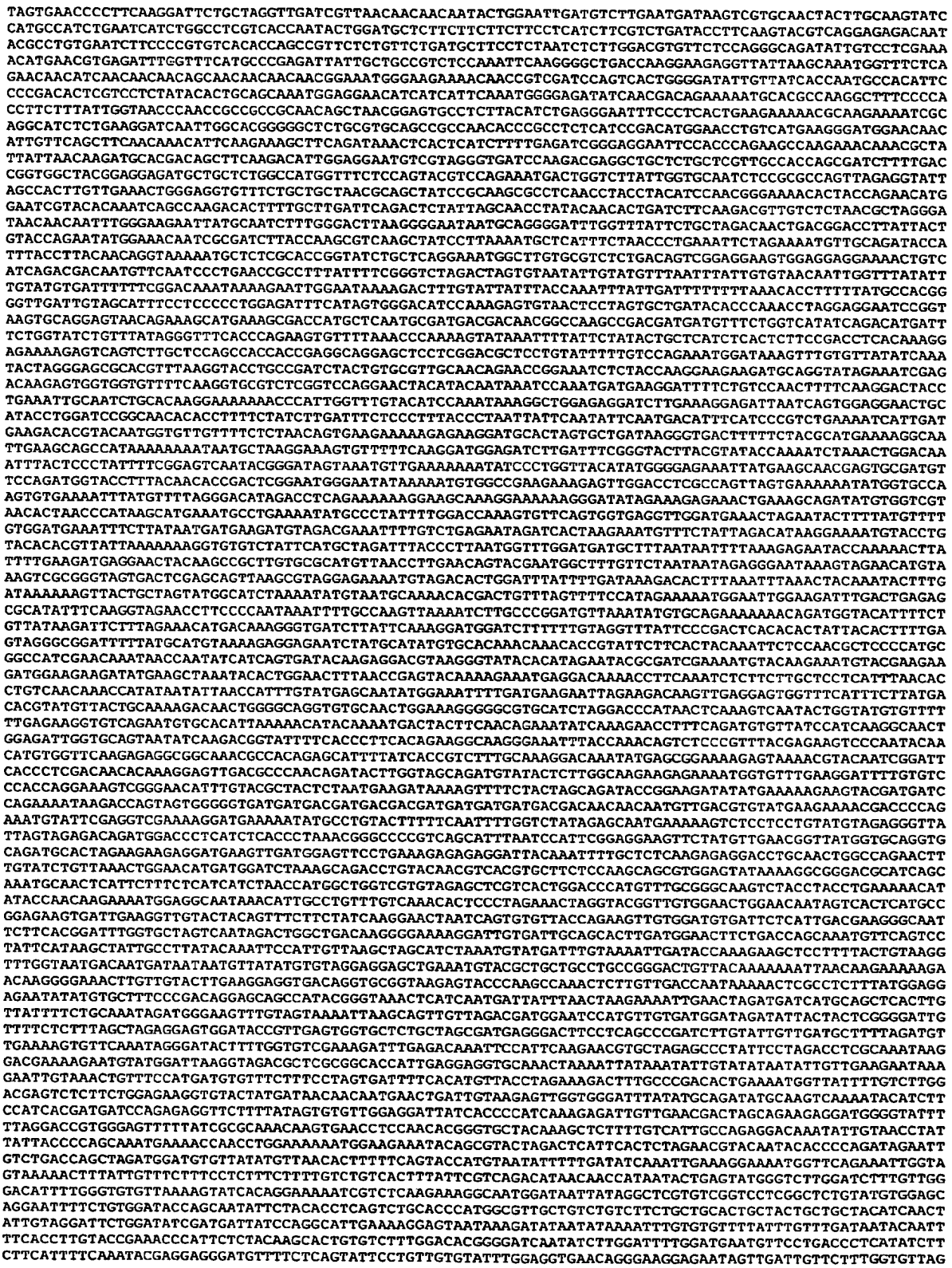


FIGURE 2, Sheet 30 of 40

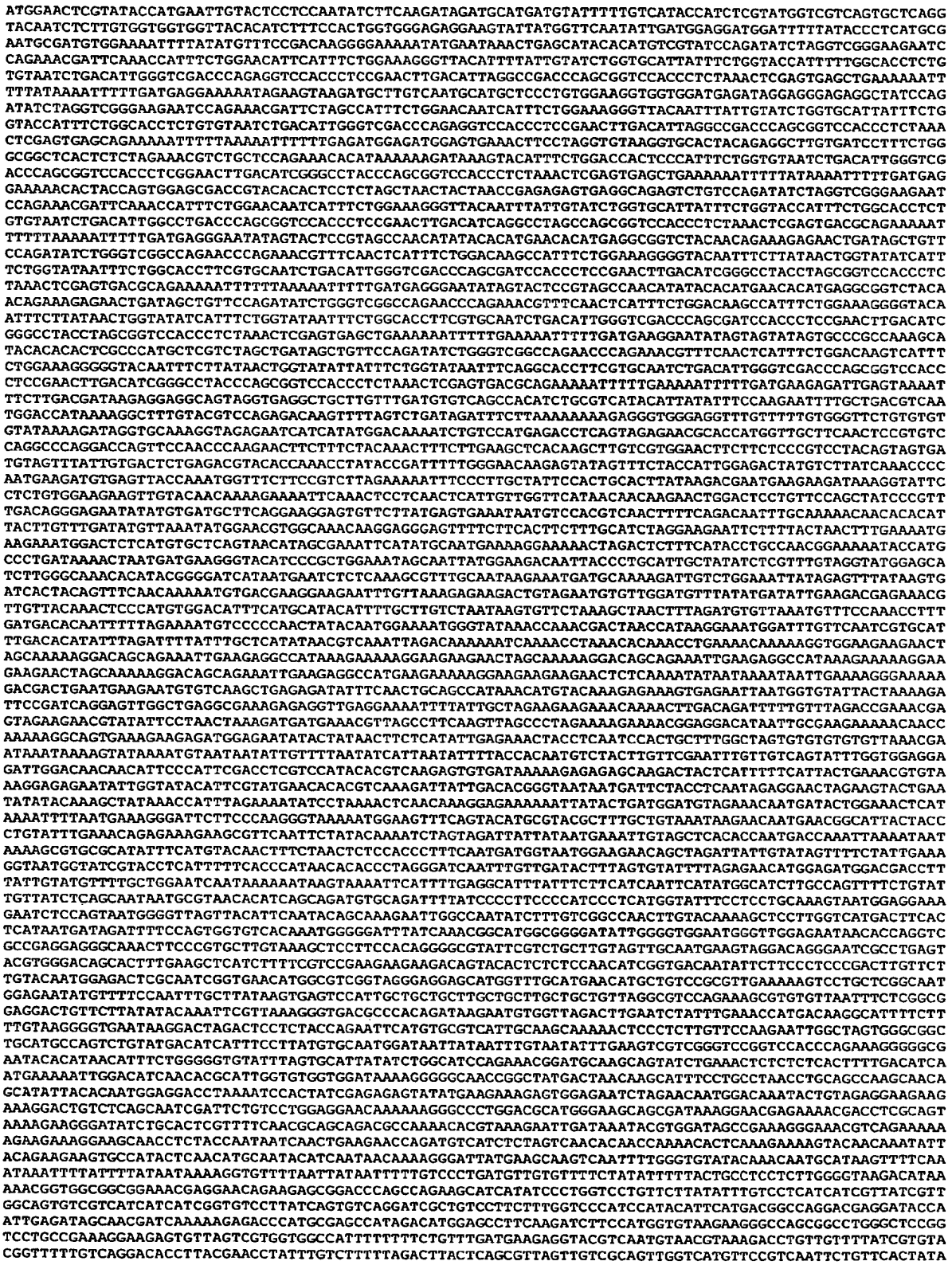


FIGURE 2, Sheet 31 of 40

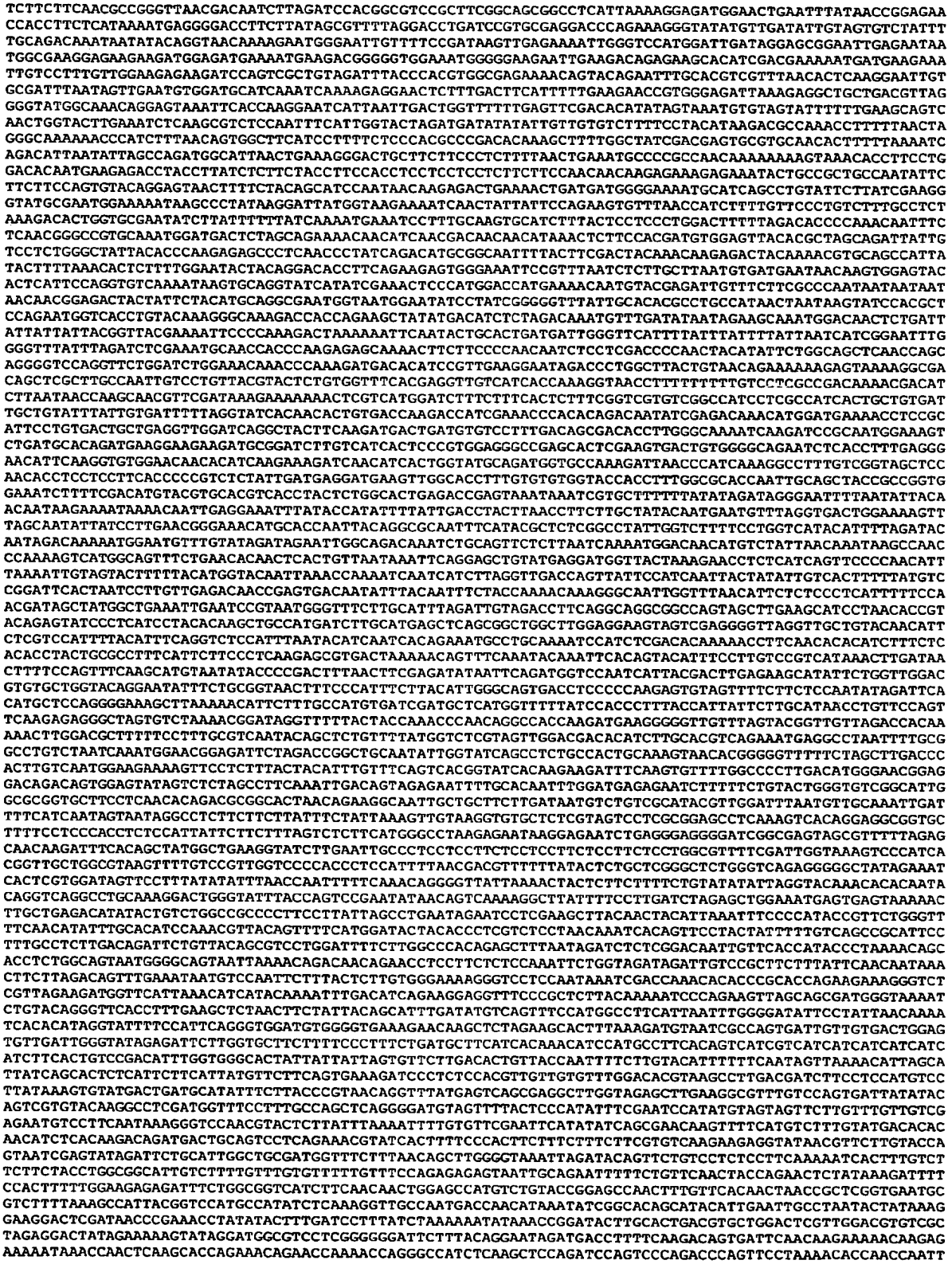


FIGURE 2, Sheet 32 of 40

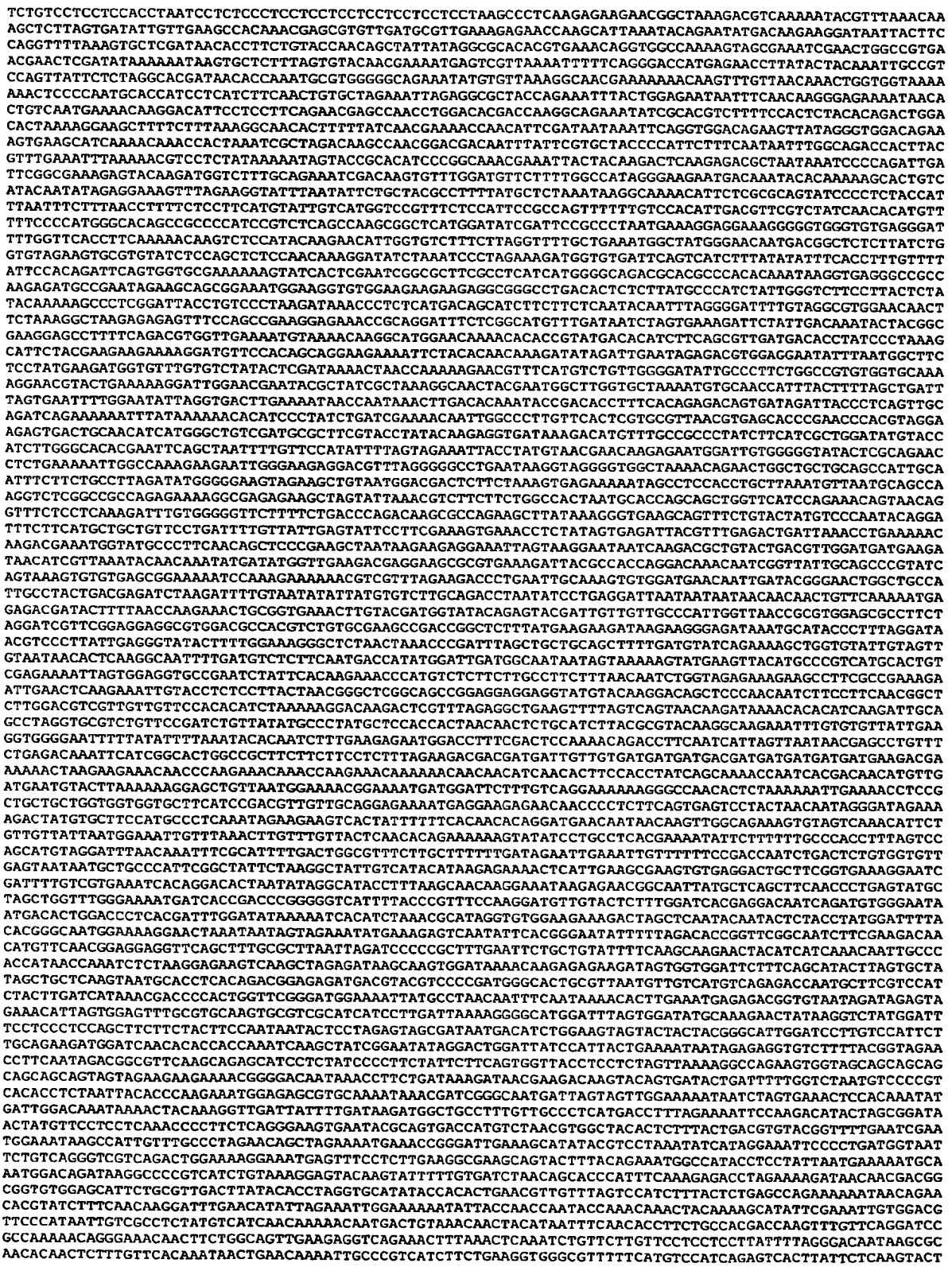


FIGURE 2, Sheet 33 of 40

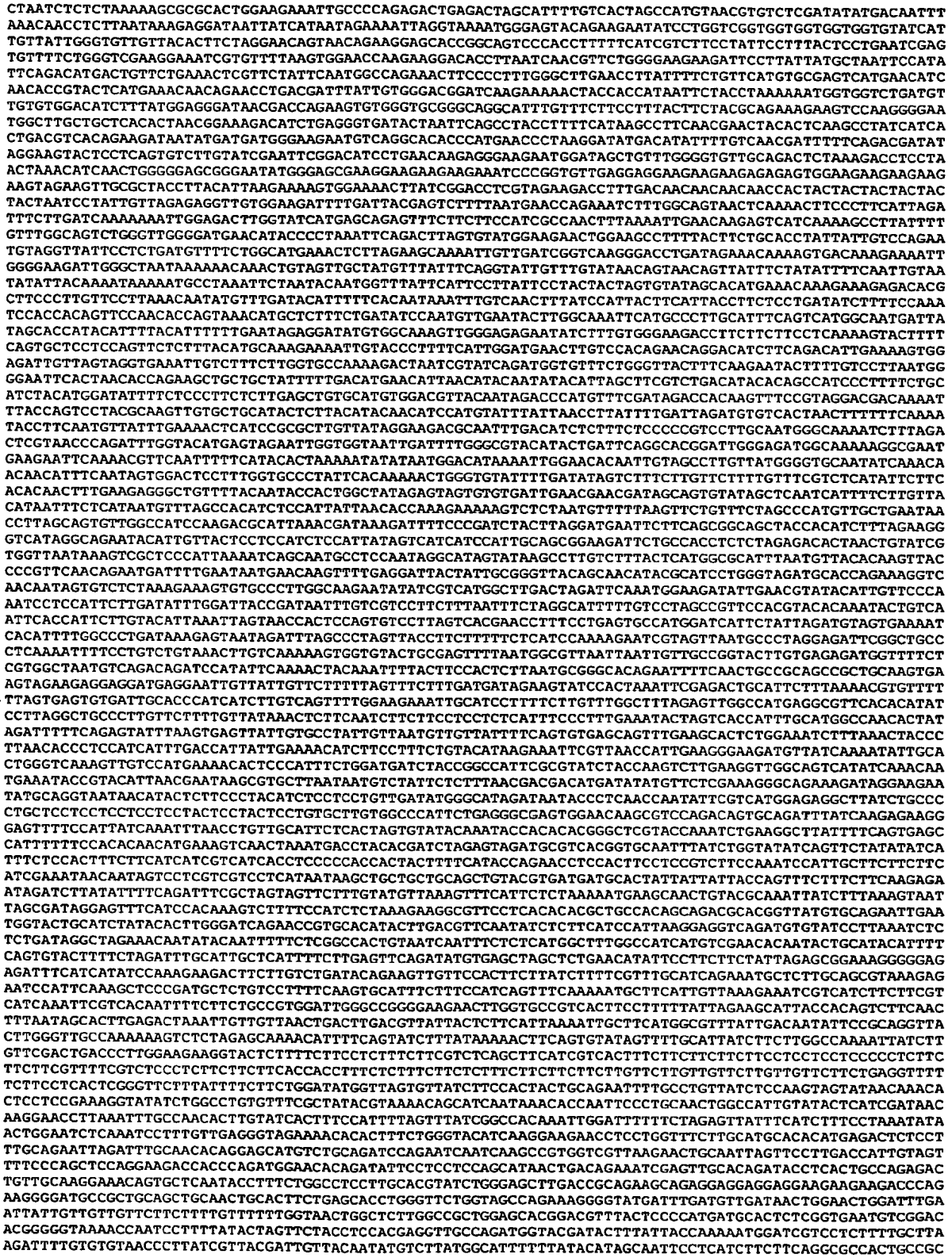


FIGURE 2, Sheet 34 of 40

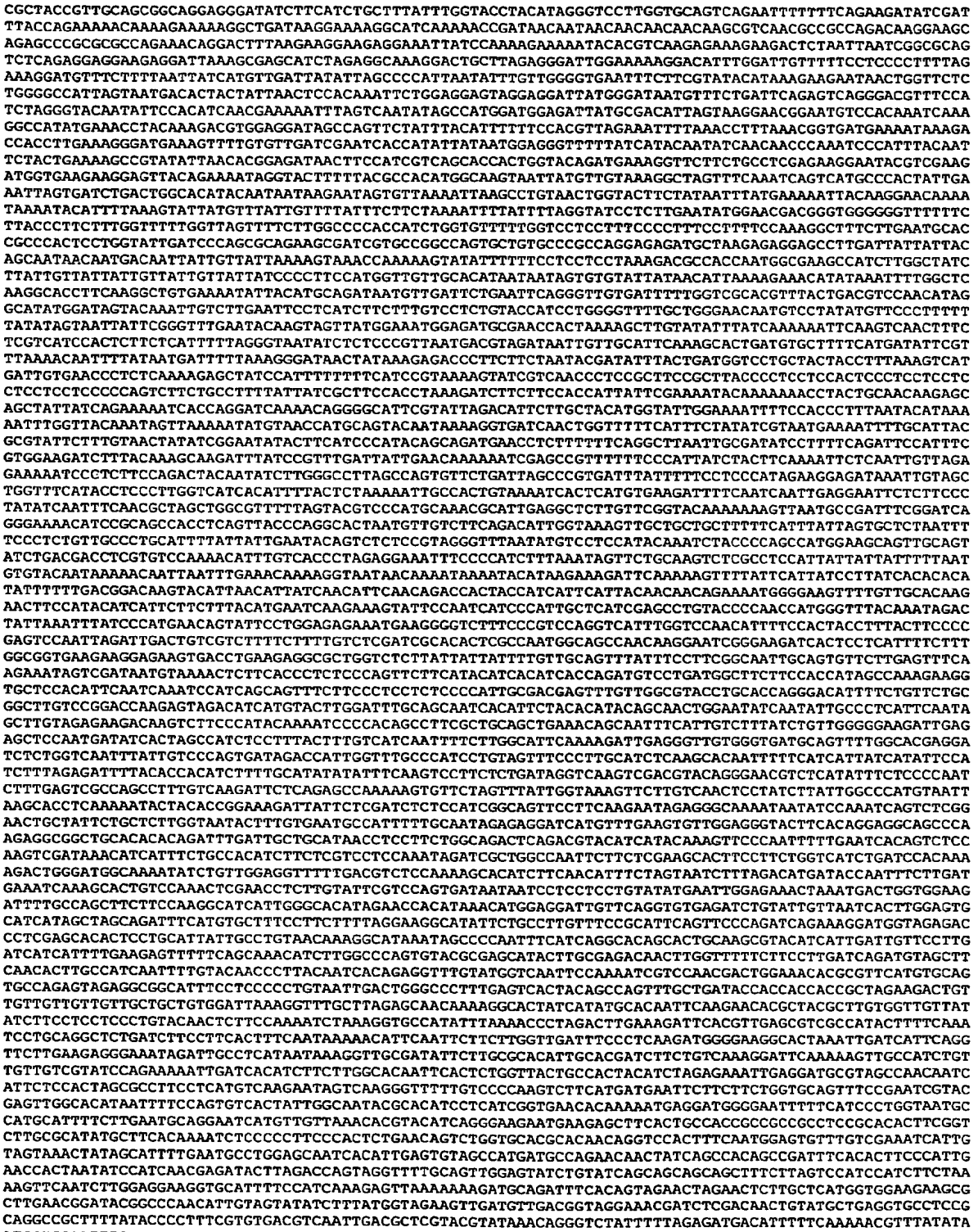


FIGURE 2, Sheet 35 of 40

TCTGACATTGGGTCGACCCAGCGGTCCACCCTTCGAACTTGACATCAGGCCGACCCAGCGGTCCACCCCCTAAACTGGAGTGAGCTCAAAAAATTTTTGA
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ATCAGATTCCAGAAACGTCTATAACCATTTCTGGAACAGTCATTTCTGGAAAGGGTTACAATTTCTTAGATGTGGTACAATAACTTACCATACATTTCTG
GTATCTTCGTGCAATCTGACATTGGGCCGACCCAGCGGTCCACCCTTCGAACTTGACATCAGGCCGACCCAGCGGTCCACCCTCTAAACTGGAGTGAGCT
CAAAAAATTTTTCAAAAGTTTTTGAATCGAGGATGAGGGTGAAAACCTGGTAACAGAAGGCATGTCTACGACGGCTTCTGGTTAGATCGAGCCGGTCCAG
AAATGGCTGTCCAGAAATCTGGGTCGGCCAGATTCCAGAAACGATTCTAACCATTTCTGGAACAGTCATTTCTGGAAAGAGTTACAATTTCTTAGATTTG
GTACAATAACTTACCATACATTTCTGGTATCTTCGTGCAATCTGACATTGGGTCGACCCAGCGGTCCACCCTTCGAACTTGACATCAGGCCGACCCAGCG
GTCCACCCCCTAAACTGGAGTGAGCTGAAAAAATTTTTCAAAAGTTTTTGAATCGAGTAAGAGGGTGAAAACACCCTCTTGAAAGGCACGATCTGGATGG
TGTCGTCCGTTCACTGCTGTTCCAGAAATGGCTGTCCAGAAATCTGGGTCGGCCAGATTCCAGAAACGTTTCTAACCATTTCTGGAACAGTCATTTCTGG
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GTAGGAGAAGGTACGCACGCATACTGGCGGCACATGCCTCCAGAAATGGCTGTTCCAGAAATCTAGGTCGACCAGAATCCAGAAACGTTTATAGCCGTTT
CTGGAACAGCCATTTCTGGAAAGTGTTATATTTTCTCGCATCTTGTACATTAACTTGATTATGGTATAGTACACCTCTCTGCAATCTGACACTGGGTCGA
CCCAGAGGTCCACCCTCGGAACTTGACATCAGGCCGACCCAGCGGTCCACCCTCTAAACTCGAGCGACCCTAAAAAATTTTTCAAAAGTTTTTGAGACGG
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ATTGTGATTTGTTGTGCCCTTTTGCAAGGCATAGGATTGTACATTTCTTATAAAAAATAAAACAATATATAAAATTCAGTTGTATTTTTATTGCTCAAAT
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TCTTCCTCTTCATCTTCATCTTCTTTAGTTCGTTCTTCATTATATGCTTTAATTATCCTCAATACATTTAAAATGGTGCGCTCTTCTCGGTTAAACTTCT
GATTCTTTCCCTCACCACCAACATCGACCCTACGTCCATCCTGGTATACTGTTTCACCATCACCAGAAAAAATTCTAATAGACGGATTTTTTATAGAACG
TACAACAATGTCCACTAATGATTCTGGTTCTGGTGCTAACTGATCATCGCCAATAAAAGATAAAACAACTCCAGAAACACATGGATAATATTGCACATTG
AATTGATCATATAAAGTATTGAAGATGATAGGGTAAGATGTTGGCCCGTAGGCAGACATGATCAAACGGGGCCTGAAACCACCCTCATCTCTCATTGTAC
AATAATTTGAACACATGAATCTGATTCCTCTTTCTGTACCAGAATATAGGGGTGTGTCTTCATTGAATCTGTTTGTGAGGAAAAAGTCTCGTGCAGATAA
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ATTTGTGAATGATGTTGAAGAAATAATGACGTTTTTTCCAAGCAGGGGTTGCCTGCTGAGAGGCGTATTTTATTCACAATTTCATCCACCTCATGTTTTG
GAGTATTTTTATGCAAAGAGACGATATATACACCTTCAGCGAGTTCGCTTCTCCGTATACTTTTGATAGACTCGATAATGGACGGTATTCTTCTATAGTT
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CAGTGAAGAAAATACTCCTCAACTTCCAACAAGAATGGGCTCTGCTAACTTGAACGACCGAACTCTACTCGTGGAGGAAGGGCAAGTAAACGACTACGGG
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TGCTGGTGACTGTCATGACTTTGTTGATTGTGGTACTGGGAACTGCACCAGTTAATTGTGATGTGAGCCCACAGAGCTACTCGCCGCCGCCGCAGCCGCC
GGTGCAGTTTCATCCTTACCATTCTTCTTCCACAACCACCACTACTTCCACTACTACTACTACTACACCAACTCCACCAGATACTAAAAAAGTTGACGAC
GACTATGATGACGACGTCAATATTGGAGGGCAATCAGTTACTGTGAATAATGGAGGTGTTTTCATCAATGGAAGAAAACTCTCAAAAGAAGAAGAAAAAG
CAATGGGTATCAATACAGATAATGGAGGATTTGTTTGGAAGAATGGTGTTTTTTCTCAATATGGCAAAAAATAAAATATGGTATATTAAATATGTGTTGT
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TTACATGTGGAGATCTTGTATTAGCAACATTAGAGAAATGGGGGACAATAAAGATTATGAAACAAGACTGATTCAAAGAATTAATGATTTGGAATCAGAA
ATTGAAAATAAAACTGAATTATGTGAAAAAATCAATGAGCAGATGAAAAATACACAACTAAAATATGATAAATGTTTCGTAGAGGAGGAGACGGAAAAAT
TCCGCAAGATGGAGGAAAGAGTTAAATACCTCAAAGAGCAGGGAATCCCTCTAGACCCAGAAGAAAGACGTACAATGTTGGCTGAAATTGACAAGAGTAA
CAAAGAGTTAGATGCCCTTCTTGAGGAAAATGAACGTATAATAAAGCTCATTGATGAAGAGTTGGAAAGTATGAAATAAAATAAAAGAGTAGGAGACTTT
TCAGTTGGTGTTATAAATATATCCCTGCAAGGAGATACGGTCTCAAAAAATCCATGACTTGTCAGTAGCCACGGAAAACACACTTGAAAAATACACCAGA
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TATAGAATTATCCATTGATACATTATTGGATGAATGTGAAAACTTGCATTATGGTCTTCAAACAACTAAATAACTCTTTATCGGGCAAGTGACTGTATTT
GTACGTATGCAATTAGGTCCATATTGGTTTGCAAATAAATAATCCACACAAAACGTGTTGTTTTTTCTATATCCTATAAATTCTTGGAACGGAAGTTATGA
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AGAACCCAAAACAACTTCTACTGTTTACACTTCTGTAAAGTGTTACCTTTCTTCCATAATCAAGAGTGAAAGTAGTAGAAGTAATGTCACCTCAACCAAA
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CTCATGGATTTCAATACCATCACCTACGCCGCCAAACAACTAAAAACTTGCTTCGAAACAAACCTACGCACCCATTTCCGGACACGACAACAGAGGGCCA
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TGGTGATTTGGAAAGGGTAAAAGAAGGAACGAAAAATTTCGTGACTCTTCATAGGAAACATTTATGTGTTATTAGTGATAAGAAGAATGGTACAATTTCC
TATTCACCTGAAGAGAAATATCCGATACCCTCAATACTAAATTATTACAAGTTTCTACAAACAGAGTATCCACAAAACAAGAAAATACAGAAAATGATAG
TTGTCCCAAAACACAAACTAAAGATACACTATTGTACGTTTGACCAAACGACCATTCAAGGAATTTGTAAAGATTTGGGAGTGTGGAAGGATATGGAAGA
ACGACACAAACAATCAGAAGATATACTTTACAAGCAAGGATGGTACCTATTATTCGACGTTAAAAAGATTAAGAAATTGCGTCCAAACTGGAACTTTCAC
TCTATCCAGACGGACGGCGAAGGCGTCTCTGTACTATTTTCCAGAGAAGTGGAAGAAGTAGAGACTGTTTCCAAGAAAAGTAAGAAAAATAAAAAACCTA
GAGGAGATGAGGATAGGAGAAATTACCCGCCCACTAATGCCAAGTACGTAGTGGGTGTAGATCCGGGAAGAACTAATGTCGTTTCCTGTTCGGTATTTGA
TACCCGTCAAAAAAGGGTAGTGAGAAAACACAGAATGACTGCGAAACAATACTATCAAGAATCTTGGATGACAGATAGAAGAAAGGCAAACGAAACGTAC
AAGAAGAACAATAAAGAGTACAAAGAGGCGTTAGAGGAAATAACTAGGTACGATAATGGCGAAGAAATTATAAATGATGGTAACGGTGATACTTCTACAC
CCACTAAAAAATTCGAAGCTTACTTGAAGGTAGTGAACGAGCACTACAGGTTACTGTGGAACGAAAAGGGAAAGAAAAAGTACAGGAAAAATGCCATGAA
AGTATACTCTAGAAAACAAAAGTGCATATCTAACTTTATAGATGAATTAATCCCTAAAAGGGATAAAATTGAAGATTACCACATTGCTTTTGGGGATGCG
AAATTTGCCTGCACGGGAAGAGGTGAGCAATACGCATCACCTGCCAGGATTTTCGCCAAGAAGATAAAGGAAAGAGTCGGAGGTGATAAGAGGTTTACTT
TCGTGGACGAGAAATATACGTCAAAAGTATGCCATCGCTGCAATCAACCTTTAAATATGCTGGAGAAGGATTGTTTTTCACCGAATAAGAAAAGAAAACC
GCCGACAATAGTAACAACCACAACAACAACAACAACAGAAGAAGACGAAGAAAATGGAAAATGGAAGAAGGCTACACCTCTCAGAGAAAATAGAGATACC
AGAAGATGCTCGTCCGAAAAGACGCAATTCGGTTACAGTTCAAACCGAAAAGTATCGACAGGAGATATCTCTATGGAAACGCCAGTACCTTCTTCCACTT

FIGURE 2, Sheet 36 of 40

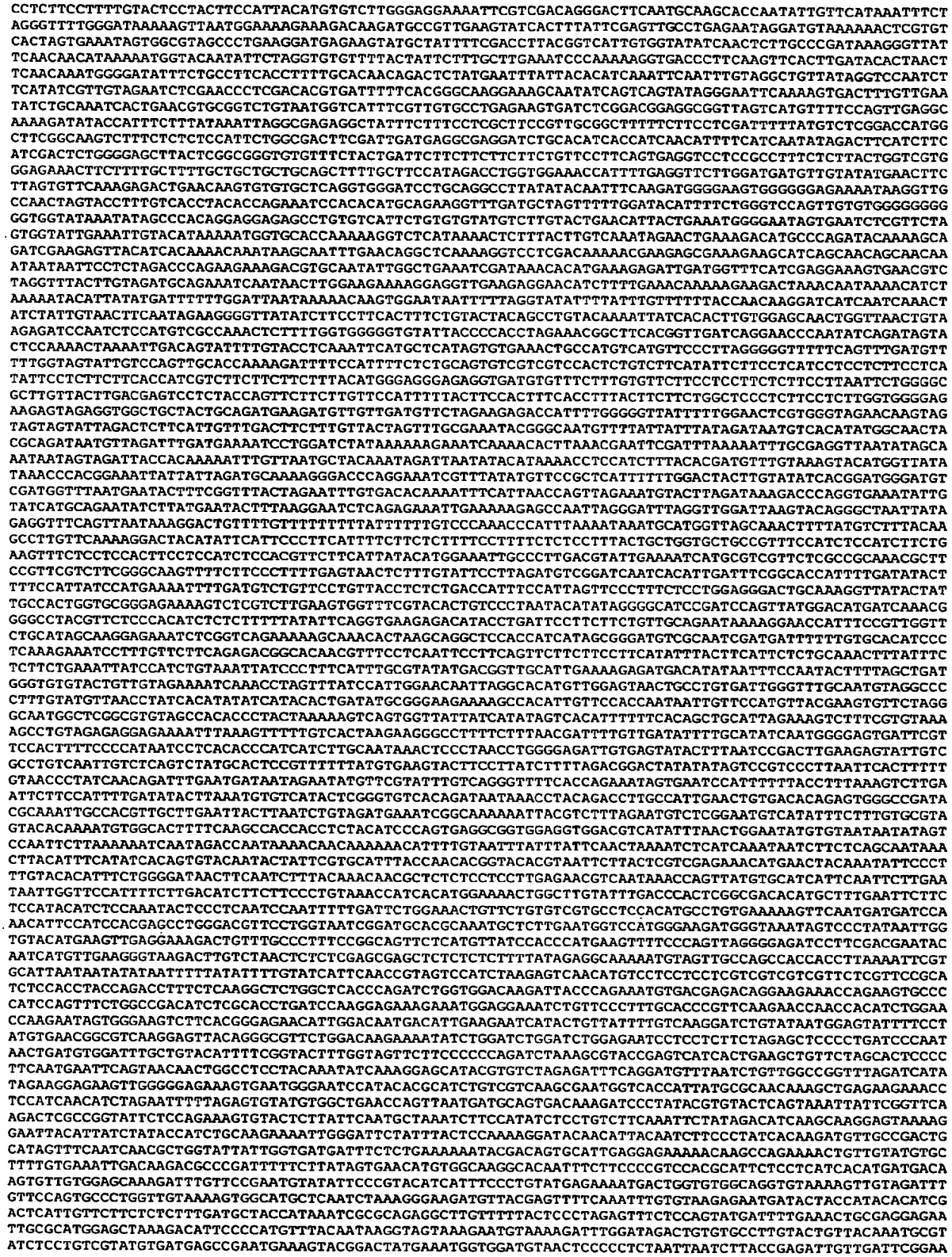


FIGURE 2, Sheet 37 of 40

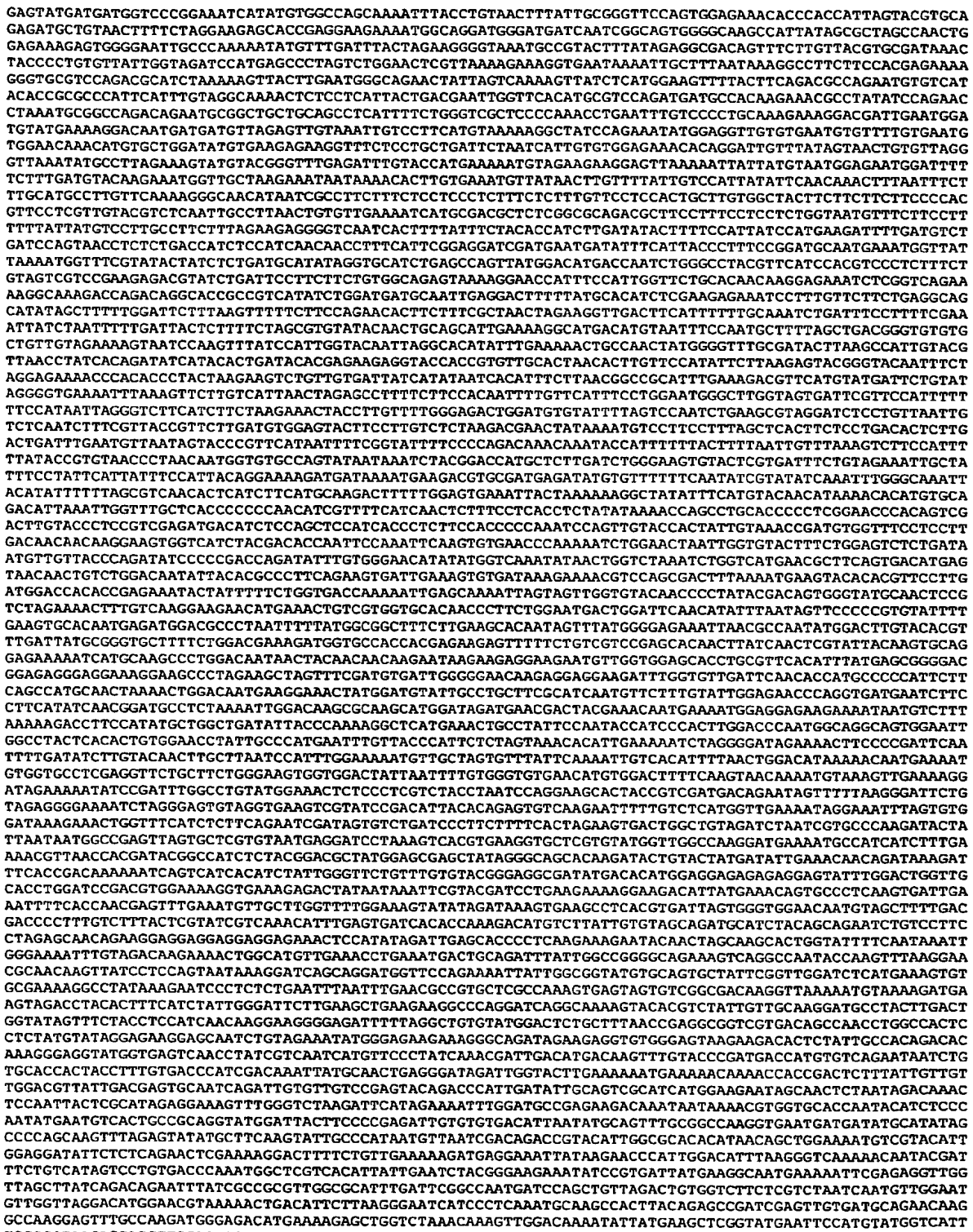


FIGURE 2, Sheet 38 of 40

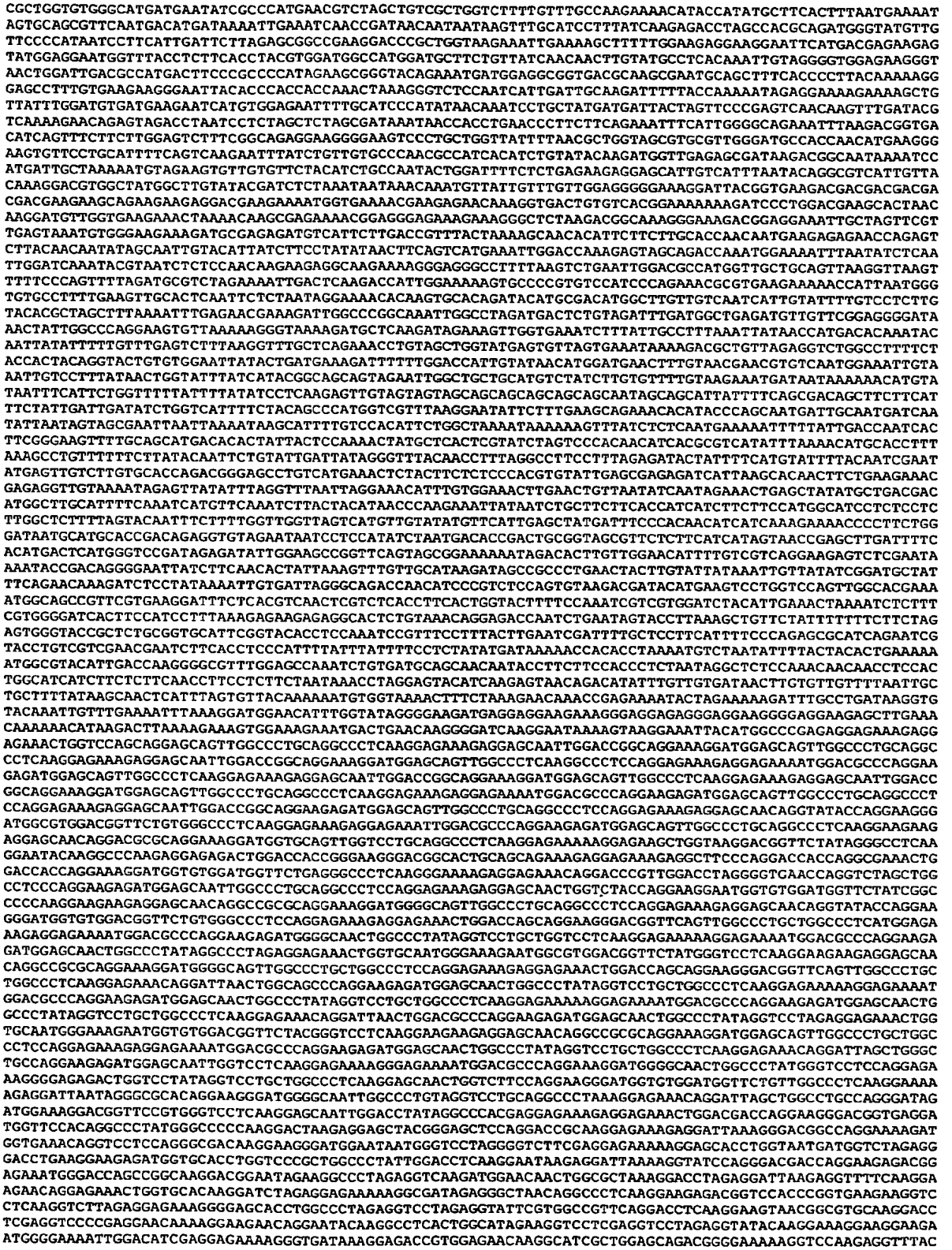


FIGURE 2, Sheet 39 of 40

GAGGAATTCGAGGCCCTATTGGTGCTCCTGGTAAGCCTGGCACGGAAGGGGTTAGAGGTCCTAGAGGGGTGAGAGGTGTTCCTGGCTATCCTGGCGCACA
AGGGGAATTAGGTCCCCAAGGACCAACAGGTCCTCAAGGGCCAGCAGGTCCTCAAGGGCCGATGGGGCGTACAGGAGATACTGGTCCCATGGGCCCTCCT
GGAGCAGTGGGACCAAGAGGAGAGAAAGGAGGTAGAGGAAGAAAGGGAAAAAATGGCCCTAAAGGAGCGGACGGAAAAGATGCCGTAAATATCATACAAA
AATATTCAATCACCCATGCTCGTGCAGAGATAATGTGGGAAGGAAATGAAATCGGAGAAGCATACATTGGAAGATCTTATGGAACTGATACAATCCCTGT
GATGATAGAAAATAGAATAGGGATGACAAATGAGGACAAAAAAAACGAATATTGTATACAAGTAATGACAATGCACTCAATAACAACTAGAGGAAGAACA
TCGGGTGTTTTTGTGGTAAGCAATAAGACAGATTATATCCTTTTAGTTACTTTACTGATGCCAGAAAGTGTTTCCTGTAGAACAGATGTCAGTACAAATG
CGAGGTCAGAGAGGGTGAATGCTGTTAGAGAAAGAGAAAGCAAATCGTACAGATTTATTAGGCCGTCTGACCAATCTATAGGTACTCATTCACGTTCAAA
AATTGCCGTGGTAATGTATCCAGACGCAAGCATGAGTTACTCAGTTGATACATTAGACGCTGATGTGGCGCGAAGAGAAACAACGTCTGTGCTTTTATTA
GCAGAAACCATACACGGGGAAAAAGATAGAGGTTTCTATGCTGATAGAGGAACTGTAGGGAGGTTGATGGTACCTCCCACTGAAGAAGAGTTATTGGTAT
TGCAAGC
(SEQ ID NO:1)

FIGURE 2, Sheet 40 of 40

CT1035
Nucleotide
Genomic coordinates:
Start: 130589
Stop: 131444 (SEQ ID NO: 2)

Amino Acid
MAAAKMDAILADINGNDTDLSKLITDVIQKRAKAVMDRNRAKMDMNRRVDEAIQEAVAAK
KQKALVVFDKLVEETDSGQSVPPTLSGSDYDAWVDRAMPSHIELVESVEGDSLYDKLPPF
NVQDIDDQIGDEIDTPISYLAMVVVKVDCETGDIEEEYNLAPTFGVTQNNKIYRDERDQI
FTKADKSVRIFKLAKLDSISGKSRQLTYAVKNNNEYTEFVCSVFAEFESDSDTTKSGIGI
REYDKPKNEFEYEEREIFTFFIPIQPAGTKLLLYFLVDVRSRII
(SEQ ID NO: 3)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
Q65326 (Q65326) DNA POLYMERASE (FRAGMENT)	36	0.31
MYSB_CAEEL (P02566) MYOSIN HEAVY CHAIN B (MHC B)	34	1.6
O02244 (O02244) UNC-54 PROTEIN	34	1.6
O04327 (O04327) CELL DIVISION PROTEIN FTSH ISOLOG	33	2.1
Q04009 (Q04009) MYOSIN HEAVY CHAIN	33	2.1
O02077 (O02077) COSMID C48E7	33	2.7

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 1 to 765 of CT1035: this corresponds to nucleotides 130649 to 131413 of the genomic reference sequence.

TaqMan Primer/Probe Sets:
5'start=350
5'stop=373
3'start=405
3'stop=427
5'primer=TCCCTCCTTTTAACGTACAAGACA (residues 350 to 373 of SEQ ID NO: 2)
Tm5=57.95
3'primer=CCATGGCAAGGTAAGATATTGGT (residues 405 to 427 of SEQ ID NO: 2)
Tm3=57.97
probe1=CGGTGATGAGATAGATAC (residues 387 to 404 of SEQ ID NO: 2)
probe1start=387
probe1Stop=404
direction1=Forward
Tm1=69.08
score1=1.91
length=78

CT1037
Nucleotide
Genomic coordinates:
Start: 131480
Stop: 132941(SEQ ID NO:4)

Amino Acid
MFVISIATSLVLFFFLLFVSITILDGAKTIDSQPFRKRRKRKRYRTSESGDGIDGGTGTT
NGGGGGGGEGGGGGTNGNGTGTTNGGGGGGEGGGGGTNGNGSGTTNGGGGGGEGGGGGTN
GGGNGNGGGNGNGNGGDTDTDDFEPTPALLKERLLNSISSKPKEYYEAFVSAEVETAL
QLSRDDSTQTIIIDDDQLELDASDTLQGKPRDYLFKLAGVSSAFLEGTTIRKAEDRARNI
NEEEIAQTILSQLREKHINDEYDGKYATPEERADFSNSLNLVTKYTNHEVGLLVGETIEK
AFPHEIEFERCIILVEDFNSGTITSNTMQYRSNAYKIRVVEGSTTDPGEVVPDDCLVFAV
VVNKEQHSLEISATNRCQDICFVIIPRLSAIGKNATMVIRKGDEIKQETYLFVANKNDTT
HFSIITDKDESVGIELNMLIFSERILPTLSDPATVPRPLTDANVLSAYGKRLGVGAFTDK
NLLSSQ
(SEQ ID NO:5)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
O65514 (O65514) PUTATIVE GLYCINE-RICH CELL WALL PROTEIN	120	3e-26
Q21835 (Q21835) R08B4.1 PROTEIN	112	6e-24
Q43522 (Q43522) TFM5 GENE	110	2e-23
O53553 (O53553) PGRS-FAMILY PROTEIN	108	1e-22
O65450 (O65450) GLYCINE-RICH PROTEIN	107	2e-22
GRP1_PHAVU (P10495) GLYCINE-RICH CELL WALL STRUCTURAL PROTE	106	3e-22

Comments:

EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 392 to 1365 of CT1037: this corresponds to nucleotides 131892 to 132865 of the genomic reference sequence.

TaqMan Primer/Probe Sets:
5'start=723
5'stop=745
3'start=792
3'stop=811
5'primer=TGAGGAAGAAATTGCACAAACAA (residues 723 to 745 of SEQ ID NO: 4)
Tm5=58.39
3'primer=CCTCGGGTGTGGCATATTTT (residues 792 to 811 of SEQ ID NO: 4)
Tm3=58.37
probe1=CAACGATGAATACGATGG (residues 774 to 791 of SEQ ID NO: 4)
probe1start=774
probe1Stop=791
direction1=Reverse
Tm1=68.98
score1=1.98
length=89

CT1038
Nucleotide
Genomic coordinates:
Start: 132993
Stop: 133896(SEQ ID NO: 6)

Amino Acid
MGDKQKVEQLLRELKAEANDDWLSANVDPIVERFVTTKSDETAQVVKQAVDEKYDELLED
KVEEMRPDIINEASETYDKLAADMIREVDTSSVIAPAIAGTVARTINNLRDKRKEYEKRL
WTLAYKPWRRYVQAITVMEFRLSYKDLTVHANSDTYLTFPFLRIKKIAYINNDRASPVNC
SLSVSYPNKSEWGNDNGVGRKVDIHIRRNDLQEKDLYLSVICMLDTDFSGYDKAVEVDAH
KFHFEAGNRTMFLPKTSNLFNRSHIVNSKICTIVFPPASASSASTTELDNVYYRITCTCS
(SEQ ID NO: 7)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
RESA_PLAFP (Q26005) RING-INFECTED ERYTHROCYTE SURFACE ANTIG	38	0.12
Q9X9G6 (Q9X9G6) HYPOTHETICAL 35.5 KD PROTEIN	37	0.15
CAA21397 (CAA21397) ORF 74	37	0.15
Q9ZFZ9 (Q9ZFZ9) HYPOTHETICAL 21.1 KD PROTEIN	37	0.15
RESA_PLAFF (P13830) RING-INFECTED ERYTHROCYTE SURFACE ANTIG	36	0.26
Q9ZH03 (Q9ZH03) LAMBDA HOST SPECIFICITY PROTEIN J	36	0.45

CT1039
Nucleotide
Genomic coordinates:
Start: 133968
Stop: 136344(SEQ ID NO: 8)

Amino Acid
MEEESQRVQRRIGVLPEEAASQILKDTKLRVSYLGVGHWGYSVSVIKSALQKGCRRNDED
ITAWSIREAYLYYHLGLNYIENVKPAAKSLNTNMVNRIKIIAVEDTSPRSMVASNECVRT
LEKYEKGNFRQPSYLMDAAMRLVHASSSRVCSHMRALCCKEEDSDKLGGIYYANFNELET
QCVSAVNFSPIERIKHVFREIESVKLGKKSVQLLNLRSVAAYHVLRYYGDKVKDTNKKHS
GPFKRKEFEQFWGLCFKFVTQHVKTDPELRCYFNELTYAINWRRDFFCSKGFFREESLFL
TSIVELIIAMCIGDRKQFAKIQKRDLKRFNKGEEGRKEEAATFDWIEGHVKRMPQMPVWV
LDKHTNKNTHGVSFALESSMVSGGDKRWSPGVWLHSYTKMRLDSPPPPEVGQFLDQAFNT
LKREAASHCVTRNICTTTGFIKASSFTANINSEPMEIKEEIKKRKIEIKDDNTTATVTVS
ATTSSSITSTPPPTKKQKTTPSGSNKVDSIQLNNLPTLNMEDLDRVLEVHNQNSKKGVAA
TVLMKDGNKVVFKEMRKSFGWGSHQNFVQVLKDEDVCKLDYLLPCPDSGPYRGLYRCYFK
IVKDEISSTAARIEKVKWGENAMCYFISGCVTRQEGIGKIITDVRLSHMGPNKQYVYDNY
RQLIHILIFRLLTGVSDTNTSNILVGDGGNLFSVDENYVGAKDPRTALENRKIKELQLLL
KTSFKVNKVTKEDIDSCLPSWLFDTSKSDKIMNGVCNIGKNMGIGPTTLDIVKNNCTCIL
GVVNDLLYDNK
(SEQ ID NO: 9)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
Q9Y1H4 (Q9Y1H4) GAG	43	0.011
RAP1_YEAST (P11938) DNA-BINDING PROTEIN RAP1 (SBF-E) (REPRE	41	0.031
SLY1_YEAST (P22213) SLY1 PROTEIN	40	0.070
P90603 (P90603) MUC.CL-1	38	0.20
O52224 (O52224) GLUCOSYLTRANSFERASE (EC 2.4.1.5) (DEXTRANSU	38	0.35
Q20202 (Q20202) F40E10.5 PROTEIN	38	0.35

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 1 to 1092 of CT1039: this corresponds to nucleotides 133866 to 134957 of the genomic reference sequence.

TaqMan Primer/Probe Sets:
5'start=1255
5'stop=1277
3'start=1353
3'stop=1375
5'primer=AATACATTGAAGCGAGAAGCTGC (residues 1255 to 1277 of SEQ ID NO: 8)
Tm5=58.71
3'primer=CCTTAATTTCCATCGGTTCAGAA (residues 1353 to 1375 of SEQ ID NO: 8)
Tm3=58.18
probe1=TAGTCATTGCGTAACGAG (residues 1278 to 1295 of SEQ ID NO: 8)
probe1start=1278
probe1Stop=1295
direction1=Reverse
Tm1=69.03
score1=1.96
length=121

CT630
Nucleotide
Genomic coordinates:
Start: 249215
Stop: 247358(SEQ ID NO: 10)

Amino Acid
MALKDAFTERLVVNKVGSGTDMAPVVEDDRQKSLFQKVENLYRVLVVEQKNSAITLSGNK
NTNKRQCRQVEEDKVIFEGEDRTVSNLPQAVKETIAANAESILDYWYKNVIPLLDTKKER
SGKSDTFLRTAVICLVRCCVSYKDMKTCSLIYEFEHKILNKSTLDPLLKDILDNKQELLH
MDSKYGSKTTSPELAKETIEALYTTVYNHWTNAFKLYQASLTHKPVTGKKYASVIHFIRT
WRKIVKAYVSKHNNVERDLSLKNIMKNESADNANVLTIEKMYKKIGNSVKNTNNNSAHQM
SDSEDDDDDDDDCEGMDVCDEASEREKKHQESLYPINTPVTTITGDYIFKVLLELVLSP
HIHPEWKIPMCDFVNRNIPKLMKAMETDISNAVIEVRASKVNPVQILPIAANFWDFCKSG
KPPSDVKFCMMFNEPSSNETLSSGAGVFGRFIGGPFSHKSKELDIISNCLRSLLLNKEAD
NLSTRIWREGGSVVCFNYCPITARGAVLGYGEQLSERSIKALWAKKIQDAVTESVKRQRN
AADKNSRNCDLLGDEGVVSMKTVTFGCANMLKTQNGMGKFNVVVSFEDSIQANKEGAARQ
YMSQQVFTHSFPALDQGK
(SEQ ID NO: 11)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
O97318 (O97318) PFC0865W PROTEIN	45	0.002
YB00_YEAST (P38114) PUTATIVE 126.9 KD TRANSCRIPTIONAL REGUL	44	0.003
Q08281 (Q08281) CHROMOSOME XV READING FRAME ORF YOL138C	42	0.010
Q92271 (Q92271) 12.8 KBP FRAGMENT OF THE LEFT ARM OF CHROMO	42	0.010
O62235 (O62235) F36F2.3 PROTEIN	41	0.018
Q83970 (Q83970) (CPV)	41	0.023

CT631
Nucleotide
Genomic coordinates:
Start: 264975
Stop: 259164(SEQ ID NO: 12)

Amino Acid
MGSKRPCSSGQEPVTKKQKKNNNNNSNPVPVINIKSYPFLATRTQVLRSAVAAAAASPSG
SSSSSSSSASAVKLPDTCKEARKVLSTVSLQQSLAVRYLCNSISVSYAGGGISVFHLGGL
PGAGKTTMVKELIAVLNDHGLIDSGSADMLLCCKSNSAKESLMCACKKPGGSSLMYPESV
FSTLNKGFEIPVIFRKDEITLEKIQFVADKLKWKVIQVLANLRFLVIDEYTMASCRELVF
IDAVLRIAKHRPDIPFGGVFVILLGDNRQNSAVVEDNTNHIQKKIKNPSEEEKPQKNNKN
NKNKKKKKEKKEKGGEEEEGDENEEEEGEEEEEEEESDDEAETKKEEEKSTFFQGSVEQD
NFGQEDNAKLYTEVFIKILKMFCSRDFFGNPSNLRNIVNKRHEAILMKSNNVKSVNNNLV
SSAIKVEDCGNASNKKEVTAPSSSPAQSTAEENCDEFDDEEDDDFFNNEAFLKLMERNAL
EKDRASGALNGFSLRCKSISDANEKIRSGTTSVSDKKSSLDMMKSLPLSALIEEGICSEL
AHISELKKMSNANLEKYTENVCSIVFDMMAKAMREIDYSGREKLYIVSSLSERFKDTHLT
SLMDEEILNVKYVHGSDPKCIDAVPFNSAHNRASAVAACVRNAFFRDGKDFVDETPIANY
FKDNLRTVASFLENETLTYKELLAKSENIRSILLKKETGNNNSASSRTAAAAAYYEDDED
YCYFDEEEAMDLEDGGSGGSGMKSSGGGGDDDDEESGEMIYRTDIPDKLHRDASTLDRVG
HLVDFHVVWKKWLTENKPSDLVRARVWYLYTLVRMQQVKFDNGKLPSLDKSALSGRLFHS
PSEWATSTGVGVGGGGGAGADKPLHDEYWLRVLSMPISTGGDVGKSMLLPAYSSYLSALS
RTYIMSSLKRIDIIKHAYSLMYGISLFDMTANLQDLVDTRMAGRSSRNGSVFMDNFDPVQ
YFDNIFPSMVNEFLMYRKEDVFNNGQMMEGVKGSLKISRVLQTAHTENNNINNRHNNSLK
YSEKSIVLAMQMVTSISKGNERRKKIEEFITKEQGQPKDMCERLMANSKAKQEKDAISSK
TDKMMGAITLTKKHVLKNAVSNLVDTSIIKETKKNNNNSSSSSSTSLAAAAAVENSVPAL
RVEVKFVVLNMDLSDISHEKTISHKYRQQLINAIKTRSTPLFDKFTDRKILRAAESPRAL
TTILLDEKKKVTRAKSITLYQGQNVIFTTSNRMIHGTQERFVTKDTGVVTNLMYKNGELT
VFVYVERLGQKCLEIKEGRQIIGNPNIKNGGFGNNVYVQYLPFESSQAMTIYSCQGHTFF
RDTIVDLSGASTQDAYVAVTRNSNPQNLFIIQNHSVERGNLCNIKCAMSKDKAYTMPIGG
IADFNGSDFINHDTVSVSREVAESSAAMDDDYNGDGGVTMYSAYDPSKDVVAAAEEFILS
RSGKSLSFNASWMANTAKVIQQHGLETELKNIRDFFFGVNNGDVAKHYEKLCNKKMIELY
TAIVRSITHYSIASGIVKQPSSKLCEEYETKQKNKKDYIKIHPVFVNRAPKESTIEMLLF
DIAPHNKATIVFQFYVHYIFLVYEKLNVLNSSFAFLPSPNPCLNQYVRPKSITTNSTHVP
NLGYESKDFAHCKDGGERDVKLRLPITSADEFSNNIEGILKKVSDTSNQNKVNKYMDVVC
KSMQHNLRRTGKFCRPTETCGLSKHGSIVTSTCTAQEKGENIHVDAEKGWLCMSDEANVY
CMLMFMSKIAAASGVSEFPIKDKSILESNPETPSDTISLLAPRKTISPTNNLHFSMSEDV
LFCGQVHPMKRVQFSLHVKRTGGALKSTFEEEEGLPTKIFSPNFATYPLFKKCKMYGAII
IAMTEMQGHEFAKYSTLDIRKSMFTGVGTVVDLEKISGEGNEVMDKVDKFIVKNVSNILF
KEQGKRVSFFVSCAIH
(SEQ ID NO: 13)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
Q9YTL7 (Q9YTL7) ORF 48	68	5e-10
O35788 (O35788) CYCLIC NUCLEOTIDE-GATED CHANNEL BETA SUBUNI	68	5e-10
NAB3_YEAST (P38996) NUCLEAR POLYADENYLATED RNA-BINDING PROT	68	8e-10
Q07034 (Q07034) RNA BINDING PROTEIN	68	8e-10
O96229 (O96229) HYPOTHETICAL 78.6 KD PROTEIN	66	2e-09
O96134 (O96134) SER/THR PROTEIN KINASE	66	3e-09

Comments:

EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 1 to 830 of CT631: this corresponds to nucleotides 259304 to 260133 of the genomic reference sequence.

TaqMan Primer/Probe Sets:
5'start=2408
5'stop=2429

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3'start=2489
3'stop=2509
5'primer=GAGCCCGTGTGTGGTATTTGTA (residues 2408 to 2429 of SEQ ID NO: 12)
Tm5=58.49
3'primer=AGCGTCCAGACAGTGCAGATT (residues 2489 to 2509 of SEQ ID NO: 12)
Tm3=58.56
probe1=CACTAGTGAGAATGCAAC (residues 2432 to 2449 of SEQ ID NO: 12)
probe1start=2432
probe1Stop=2449
direction1=Forward
Tm1=68.99
score1=1.99
length=102
```

CT632
Nucleotide
Genomic coordinates:
Start: 268485
Stop: 267717(SEQ ID NO: 14)

Amino Acid
MAGVDLYGGHIKPYGETVFNNKMQGNRGKIRALINEKAAATLPMSEDNISAWVTEVAADV
FPDPKSALTFFVPNKSLNAFAWDVLKTPASVEIDIGKRIPQLIENLHMSDFTVAIFRVKC
DDQGRYETSYNLSPSMGGKINHGLIRTLAKAQDIVVWKRDFSLTIENFEVDNGKKRLDFL
FNNQTDKSCFVKIFHEMESEKDIAIKPEKRGSSAVWDEVYSDIVTKNTRNAKFSLRYRNE
KPVDHLLLYCMVTYF
(SEQ ID NO: 15)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
O97036 (O97036) PLC-BETAH2	34	1.5
O45329 (O45329) F09C6.2 PROTEIN	33	2.5
P97868 (P97868) PROLIFERATION POTENTIAL-RELATED PROTEIN	32	5.6
P70287 (P70287) RETINOBLASTOMA BINDING PROTEIN 6 (PACT) (FR	32	5.6
AAD49229 (AAD49229) EHEC FACTOR FOR ADHERENCE	31	7.4
CAB55629 (CAB55629) LYMPHOSTATIN	31	7.4

Comments:

TaqMan Primer/Probe Sets:
5'start=378
5'stop=403
3'start=452
3'stop=477
5'primer=TGAAACCAGCTACAATTTATCTCCTT (residues 378 to 403 of SEQ ID NO: 14)
Tm5=57.68
3'primer=CCTCTTCCAGACTACAATATCTTGGG (residues 452 to 477 of SEQ ID NO: 14)
Tm3=59.43
probe1=TCAGAACACTGGCTAAGG (residues 434 to 451 of SEQ ID NO: 14)
probe1start=434
probe1Stop=451
direction1=Forward
Tm1=69.15
score1=1.84
length=100

CT633
Nucleotide
Genomic coordinates:
Start: 266790
Stop: 266442(SEQ ID NO: 16)

Amino Acid
MASPLVASLGGGKNILFGLLLITIIVIVIAVIIIKAPLLASLLAGTALAGTIASALGSIP
GVGGAFKKAFGKGKGKGGPKTPDGGAKKTNQKPKKGKKKPPTRRSIFKRIPKIKF
(SEQ ID NO: 17)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
Q02391 (Q02391) CYSTEINE-RICH FIBROBLAST GROWTH FACTOR RECE	36	0.092
Q91019 (Q91019) MUTANT CYSTEINE-RICH FGF RECEPTOR	36	0.092
Q69526 (Q69526) GLYCOPROTEIN B	36	0.12
Q9XZ15 (Q9XZ15) HYPOTHETICAL 29.3 KD PROTEIN	36	0.12
Q14113 (Q14113) AORTIC CARBOXYPEPTIDASE-LIKE PROTEIN ACLP (	35	0.21
P79922 (P79922) MODIFICATION METHYLASE (EC 2.1.1.73) (CYTOS	35	0.21

FIGURE 3, Sheet 10 of 160

CT634
Nucleotide
Genomic coordinates:
Start: 283360
Stop: 282673(SEQ ID NO: 18)

Amino Acid
MVSSRTSTTSSSAVAATSTLLPTKRKREPEEVKVKVEVKMEQEELVEDSSSNKRPRIKEE
KEEEHKETHHLSLPCKEEEDDGEEEEYEEEEDEEEYEDRVDDDTAEKMENLLVQLDNTTK
NIKLKNPLREHDMAVSHYEHEFEVQNTVNFSFGVLSDIGFLINREAVSRWGNTPPPKEFG
DMEIGSLTVNQLLHKCDNFVQAVVQKVKEDITPSIEVTIDSLIDDPCW
(SEQ ID NO: 19)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
O35788 (O35788) CYCLIC NUCLEOTIDE-GATED CHANNEL BETA SUBUNI	60	2e-08
GARP_PLAFF (P13816) GLUTAMIC ACID-RICH PROTEIN PRECURSOR	57	8e-08
Q9YTL7 (Q9YTL7) ORF 48	56	2e-07
O94922 (O94922) KIAA0835 PROTEIN	55	3e-07
O08995 (O08995) MYELIN TRANSCRIPTION FACTOR 1	55	3e-07
Q93424 (Q93424) HYPOTHETICAL GLYCINE-RICH 37.0 KD PROTEIN E	55	5e-07

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 575 to 1 of CT634: this corresponds to nucleotides 282678 to 283252 of the genomic reference sequence.

TaqMan Primer/Probe Sets:
5'start=210
5'stop=231
3'start=287
3'stop=308
5'primer=CCTCTCCCTCCCATGTAAAGAA (residues 210 to 231 of SEQ ID NO: 18)
Tm5=58.19
3'primer=TCGTCGTCCACTCTGTCTTCAT (residues 287 to 308 of SEQ ID NO: 18)
Tm3=58.40
probe1=AAGAGGAGGATGAGGAAG (residues 266 to 283 of SEQ ID NO: 18)
probe1start=266
probe1Stop=283
direction1=Reverse
Tm1=68.99
score1=1.98
length=99

CT635
Nucleotide
Genomic coordinates:
Start: 285773
Stop: 284075(SEQ ID NO: 20)

Amino Acid
MARSVGLLSVTPEYDTFKYIKMEEFKTLKVKNGFTISGENPDKYEHILLSFKSVDRVTKS
ELRDGLYIVRLKDKEVLHIKNGVHRLRQLTGDNTLQVGLKYTHNLPRLGSLLQDDGCEDY
GEKWNESLPIDMQNINKIVKEKALLSDKNFKFSPLYRLLHERLSNAAVKKCDYMIITTDF
LVGCGYTPSHCPRTLRNMEQLLVEQCGFSSRISVYDICDRLTYKGAYIANPITGSYSNMC
LIVPMDKLGLIFYNSTHPSAKSIGNYMSSLFNATVIYANERDNLQMDNFRREIKFAENEV
NMKEEELKELRKRCAVSEEQRISLRDVHKKSSIATSRYDGGACLVFAFSDRDFSLLCRTN
GNGSFYSATEEGIRYVSSPEYKKRDVGERRPRLIMSITGSDAPICIRDSVRNHFKTRLFS
RTSGNSITFAVPPGERELMEMVREVTGTDIKIFMDNGKVYQNGAEINVIDPTSKEYKELL
KREENLPEDERKRLRRERRMIFNTSRAISMYNEERGDGGSGGETSEDGDGNGSTSSKGEK
RKREENEGNEYVVLLNKACKDIKVC
(SEQ ID NO: 21)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
Q21885 (Q21885) COSMID R09H3	37	0.32
O77336 (O77336) PFC0425W PROTEIN	37	0.42
O00164 (O00164) RIBOSOMAL RNA UPSTREAM BINDING TRANSCRIPTIO	36	0.71
UBF1_HUMAN (P17480) NUCLEOLAR TRANSCRIPTION FACTOR 1 (UPSTR	36	0.71
YPT2_CAEEL (P41880) HYPOTHETICAL 21.6 KD PROTEIN F37A4.2 IN	36	0.93
YG2K_YEAST (P53253) HYPOTHETICAL 106.5 KD PROTEIN IN CTT1-P	35	1.2

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 501 to 1 of CT635: this corresponds to nucleotides 284047 to 284547 of the genomic reference sequence.

TaqMan Primer/Probe Sets:
5'start=686
5'stop=706
3'start=799
3'stop=822
5'primer=CAAACCCAATCACAGGCAGTT (residues 686 to 706 of SEQ ID NO: 20)
Tm5=58.55
3'primer=GGTTGCATTGAAAAGAGATGACAT (residues 799 to 822 of SEQ ID NO: 20)
Tm3=58.19
probe1=ACTCCAACATGTGCCTAA (residues 707 to 724 of SEQ ID NO: 20)
probe1start=707
probe1Stop=724
direction1=Forward
Tm1=68.89
score1=1.89
length=137

CT636
Nucleotide
Genomic coordinates:
Start: 286706
Stop: 286076(SEQ ID NO: 22)

Amino Acid
MIVFVEGSPLTGKTSWVDNMRTAGKGKQSFLNFMYTNYRDYLPIFPWTIQEHLRASDYQE
RPRLVDGMFGSSLNFFTGMWRHDTEQFPESKIGLREYLEMYGEEFKACVAEWVKYKPVFH
VMVYREEDVKKMEPIIQELNDAHNWFIDVLKEERALFVKIEVIPRNVYKGNICSSCFSTS
KNYVYRVGKCTNSIVHCDMKCKFIAEKII
(SEQ ID NO: 23)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
P87968 (P87968) ENVELOPE GLYCOPROTEIN, V1-V5 REGION (FRAGME	33	2.0
P88315 (P88315) ENVELOPE GLYCOPROTEIN (FRAGMENT)	33	2.0
P88314 (P88314) ENVELOPE GLYCOPROTEIN (FRAGMENT)	32	2.7
DYHC_PARTE (Q27171) DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC)	32	4.6
O40068 (O40068) GP120 (FRAGMENT)	31	6.0
O40067 (O40067) GP120 (FRAGMENT)	31	6.0

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 1 to 594 of CT636: this corresponds to nucleotides 286111 to 286704 of the genomic reference sequence.

TaqMan Primer/Probe Sets:
5'start=239
5'stop=259
3'start=317
3'stop=335
5'primer=GGAGGCACGACACAGAACAGT (residues 239 to 259 of SEQ ID NO: 22)
Tm5=58.81
3'primer=CACTCGGCGACACATGCTT (residues 317 to 335 of SEQ ID NO: 22)
Tm3=59.42
probe1=TGGAGATGTATGGAGAAG (residues 293 to 310 of SEQ ID NO: 22)
probe1start=293
probe1Stop=310
direction1=Reverse
Tm1=68.95
score1=1.95
length=97

CT637
Nucleotide
Genomic coordinates:
Start: 300432
Stop: 299085(SEQ ID NO: 24)

Amino Acid
MGGEDSFDDRYDSDALWENEGAKSIQVKETDLEVYRMHRRAVPTLEEKNRTALRYYSDWS
PVYRVPLFSLKDGSDPHERDFSFNVDPRRFGKVPVKVRRVDVRNPSRTAAIFVPTGPGLH
VSSYTGDGMLVCPNHNFIGDLCSEIASDITIYNTSSSGRLSYATNFNSVEDNSPVGILFE
TLPDDKMFQQVSIFSATEPASNISIGPMSHVKIKLGYYDEENATAVGVIRYGGLFYTSVG
ACIIPEGVFFDDVVGNHSSMNIYNMTNQPKEIVLKEPRGEDAMEEDDGEEADYNFLGYVV
RFEHDLKMQAMSSAYSSVSIDINSSSFHKCFLIKPKYNSILQPLVSSEVVLNDLSLNTRG
REVEFHDRLPSGAQDNSYSIVKYMKIVSLKEGLKVVNPIINTELYKKKQALKVHVLNMTR
DVVGLDTSEHSFGVIVCHAAKLPEVIGQ
(SEQ ID NO: 25)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
O23592 (O23592) CARBOXYL-TERMINAL PROTEINASE HOMOLOG	34	1.6
YGA1_YEAST (P53199) PUTATIVE 3 BETA-HYDROXYSTEROID DEHYDROG	34	2.1
VILI_DICDI (P36418) PROTOVILLIN (100 KD ACTIN-BINDING PROTE	33	4.8
Q9Z5B9 (Q9Z5B9) PUTATIVE TRANSFERASE	32	6.3
Q9YUY4 (Q9YUY4) ENVELOPE GLYCOPROTEIN	32	8.2

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 3 to 1254 of CT637: this corresponds to nucleotides 299132 to 300383 of the genomic reference sequence.

TaqMan Primer/Probe Sets:
5'start=678
5'stop=702
3'start=788
3'stop=812
5'primer=CGGTGTCATTAGATATGGAGGATTA (residues 678 to 702 of SEQ ID NO: 24)
Tm5=57.26
3'primer=TCTTTTGGTTGGTTAGTCATGTTGT (residues 788 to 812 of SEQ ID NO: 24)
Tm3=57.75
probe1=CTACACCTCTGTCGGTGC (residues 705 to 722 of SEQ ID NO: 24)
probe1start=705
probe1Stop=722
direction1=Forward
Tm1=68.85
score1=1.85
length=135

CT1040
Nucleotide
Genomic coordinates:
Start: 137588
Stop: 139940(SEQ ID NO: 26)

Amino Acid
MAAAAVSGEGRISADLLLLEQLTPDGDVIRYDSEQYTKPRKIFGDKSVIETIGHFLIHNH
NQGESYQIASSVLEKFPALLNCIWNGESGGMALWKALYRAKKYRLLNSLLVHKIKNWPSV
AVIPIYGSVCDREERPIIMSEIIDKETLQTICKSDIRSLLGMMNAKHGTLGGNFLHFYAR
STKPFENFQYEAMGANAVLMAAEAIYDGFRDHGLNPSEYTFPGLESADVYGNNPVEIAIS
GDDDNMLLNLICNYGVSYEKTRGRVNRSLLDFLKMNTASKCLSVLKFVEKHFKIESNTPK
GEFEEKAETCVNCLDRNNVLTKGSEQESYKLSCGHFLHVKCLRNICIVSQHLRCEKCLKR
FDESILRKCTPNLNWWLTMPAGAGNEEEICFMRNKKLVDDFRKLLSPVSIPHFFKNSRQR
NLDMLCPYSDHTIIPNKEDPKKNEDGNRVRVNHTAISEKQNKEEEDARIKRVAVRTFTAI
REKQNKEEEDARIKRAVDMAVAAINEKNKEEEDARIKRAVDMAVAAINENNKEEEDARIK
RAVDMAVAAINEKNKEEEDARIKRAVDMAVAAINENNKEEEDARIKRAVDMAVAAINENN
KEEEDARIKRAVDMAVAATNEKNKKEEDARIKRIIDLTVDMRIQRIVDMAIAAATKKDKK
EEEKRTKREQELRADLRRAMDMVNEVQKKLEDMELEKGCNKDEAKNTSNVVSSSSVVAYS
KEIVPCLGNNNNAVIGMTSTNYSANNTKNNVFGSPHKFSFNDASRFSNIVETPKMSFNFS
FKT
(SEQ ID NO: 27)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
Q9ZU69 (Q9ZU69) PUTATIVE VICILIN STORAGE PROTEIN (GLOBULIN-	71	4e-11
Q26775 (Q26775) TB-292 MEMBRANE ASSOCIATED PROTEIN	70	5e-11
INCE_CHICK (P53352) INNER CENTROMERE PROTEIN (INCENP)	67	5e-10
YDF3_SCHPO (Q10475) PROBABLE EUKARYOTIC INITIATION FACTOR C	66	7e-10
Q26774 (Q26774) TB-291 MEMBRANE ASSOCIATED PROTEIN	66	9e-10
P91257 (P91257) SIMILAR TO C. ELEGANS UNC-89	65	2e-09

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 853 to 415 of CT1040: this corresponds to nucleotides 138912 to 139349 of the genomic reference sequence.

CT1041
Nucleotide
Genomic coordinates:
Start: 140110
Stop: 141616(SEQ ID NO: 28)

Amino Acid
MVYKGFVSPSFITIRTMTSNRPTTSPLSFSEGFSLSGDKYDTYEDILLEQFNCFKTSSPS
SARKSEIEDKTLIFQLKEGEKFHLAKGIEELREILDDNSATIEPIISPTTFNDRNELLNH
EGDISSSPLYTQIMKHISPEHDIYELDLIVGTDLLFGLGVNLRNVSKLMKKISYGTLNVV
DVCHRKFFNNRIIVNPISSSFSKNVCIIPLFSAAEEFSSLGECRDLFNGICDDVERYINS
YFFYPENTTTTTTTAPSSPEMEIADEEEQSPKTIKRNDNASRNWSGVCLIFEVFKNTYYI
INRGDRGGSFEKAVKSAISSIKEKRCKITDINGNKPRLVMVITGCYTELYFKDALKQIGE
NRRKFLKMNGNYFSLIDEQADLIEFAMSVSGAGERIFVNGLGMFQNRKMIPVIDPLTYEN
VVCGEHDIQKEDAILSVRRAIADYNDFVSKNKRGKKRSAEEENEDEDADASSSSSSSPPP
SSPPAHKKSRLPDEGEKCTLC
(SEQ ID NO: 29)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
Q26258 (Q26258) BR2.2=BALBIANI RING (5' REGION, REPEAT UNIT	38	0.12
Q23804 (Q23804) SPID PRECURSOR (FRAGMENT)	36	0.82
O97324 (O97324) MAL3P8.1 PROTEIN	36	0.82
Q99112 (Q99112) HOMEODOMAIN PROTEIN BW2	35	1.1
Q99111 (Q99111) HOMEODOMAIN PROTEIN BW2 (FRAGMENT)	35	1.1
YA55_METJA (Q58455) HYPOTHETICAL PROTEIN MJ1055	35	1.1

Comments:

TaqMan Primer/Probe Sets:
5'start=822
5'stop=846
3'start=929
3'stop=950
5'primer=AAAGAGAAATGACAACGCAAGTAGA (residues 822 to 846 of SEQ ID NO: 28)
Tm5=57.46
3'primer=GCACTCTTCACAGCCTTTTCAA (residues 929 to 950 of SEQ ID NO: 28)
Tm3=58.24
probe1=AACTGGTCTGGTGTCTGT (residues 847 to 864 of SEQ ID NO: 28)
probe1start=847
probe1Stop=864
direction1=Forward
Tm1=69.07
score1=1.92
length=129

CT1042
Nucleotide
Genomic coordinates:
Start: 141695
Stop: 142541(SEQ ID NO: 30)

Amino Acid
MAVNLDNVLVNINNKDEDLTKLVSEAIKRRAKTVFDTKNQAGFDMRRQVEAALYEAISKKK
EKAIKAFDELIQERGDEITPLTTMQYEEWVNRTITPSLTTENLLGDVEHADFLLDRMTPVS
EEDIEGFAASTFKEVSDSKTATVIVKADCETGDIDEVYNLAPSFGVTQEIKIYRSNNSSEL
DNVADSFHIYKISATDSDSGNTKKLLYGLRNKKAGYTCLCRIFAEIESDGIMANTNIGVAE
NNRDEIDENEEGKYGFLIPKQPAGAKLIIYFFLNCWTX
(SEQ ID NO: 31)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
gi\|2492980\|sp\|Q10043\|YRP1_CAEEL HYPOTHETICAL 37.6 KD PROTEIN R1...	33	0.79
gi\|401691\|sp\|Q00933\|YSCI_YERPS YOP PROTEINS TRANSLOCATION PROTE...	32	1.8
gi\|1706480\|sp\|P51892\|DNL1_XENLA DNA LIGASE I (POLYDEOXYRIBONUCL...	32	1.8
gi\|267570\|sp\|Q01250\|YSCI_YEREN YOP PROTEINS TRANSLOCATION PROTE...	31	2.3
gi\|3121979\|sp\|O07597\|DAAA_BACSU D-ALANINE AMINOTRANSFERASE (D-A...	31	2.3
gi\|6686325\|sp\|P71018\|PLSX_BACSU FATTY ACID/PHOSPHOLIPID SYNTHES...	31	4.0

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 700 to 1 of CT1042: this corresponds to nucleotides 141748 to 142447 of the genomic reference sequence.

TaqMan Primer/Probe Sets:
5'start=350
5'stop=367
3'start=392
3'stop=414
5'primer=GGACCGAATGACACCCGT (residues 350 to 367 of SEQ ID NO: 30)
Tm5=57.70
3'primer=CCTCCTTAAAAGTAGAAGCAGCG (residues 392 to 414 of SEQ ID NO: 30)
Tm3=57.66
probe1=AAGCGAGGAAGATATTGA (residues 368 to 385 of SEQ ID NO: 30)
probe1start=368
probe1Stop=385
direction1=Forward
Tm1=69.01
score1=1.88
length=65

CT1043
Nucleotide
Genomic coordinates:
Start: 142610
Stop: 143699(SEQ ID NO: 32)

Amino Acid
MTVLAVYTAPQIKKSKKRKIEDENEEEPVKTLEDFVKGRLLNAVKEKPAEYFELLISADT
EAALKTAEETALRDFVIENDSVEIDVEEVLEEKPREYVFKLAGATSETLTNTIIAEVQKK
AALITEEDITIKMLKQFRAANKDNKDGEATPEEKEDFTNNSDLVGLYLNEVVEKTTNIVI
NKIFPHEMVFERCAILIEDFDTGVVTDQAIQIPSNKYKIRLVEGDEPEVFPGDCLDLAVS
VDKINHVLKISAKNGCENNCFVIIPRFSPVGSVSSMILGSTDQVKPKTFLFLANKNDSTH
FQFTMDKQHSVGCELDMLIFSERNLRNLPDSKPRPLSDADILASYGKRLGTGVFTTENLV
DD
(SEQ ID NO: 33)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
Q26938 (Q26938) KINETOPLAST-ASSOCIATED PROTEIN (KAP)	40	0.022
O23332 (O23332) CENTROMERE PROTEIN HOMOLOG	39	0.037
Q9ZES5 (Q9ZES5) CTC PROTEIN	39	0.049
AAD45753 (AAD45753) ANON1A3 (FRAGMENT)	38	0.083
O66878 (O66878) CHROMOSOME ASSEMBLY PROTEIN HOMOLOG	38	0.11
AAD45759 (AAD45759) ANON1A3 (FRAGMENT)	38	0.11

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 1 to 982 of CT1043: this corresponds to nucleotides 142640 to 143621 of the genomic reference sequence.

TaqMan Primer/Probe Sets:
5'start=543
5'stop=567
3'start=635
3'stop=659
5'primer=CAAAATATTCCCTCATGAGATGGTT (residues 543 to 567 of SEQ ID NO: 32)
Tm5=58.37
3'primer=CTGATTTTGTATTTGTTGGAGGGTA (residues 635 to 659 of SEQ ID NO: 32)
Tm3=57.33
probe1=GACTGATCAAGCCATTCA (residues 615 to 632 of SEQ ID NO: 32)
probe1start=615
probe1Stop=632
direction1=Reverse
Tm1=69.01
score1=1.98
length=117

CT1044
Nucleotide
Genomic coordinates:
Start: 143759
Stop: 144689(SEQ ID NO: 34)

Amino Acid
MSSSSSETPKTSTDTGEERIKDIVNALDNNGEWLSSYIDPIINNHISRKTAETVQKINQE
VDERYDRKIADKINEIKSSIFTSAQTMYDQYAIDTFQEGKGANGTGPVMGPVNTVIDTTL
NKMRGNMLEYAEDMWDGDDWKRFSSSMTTLEFDLSYSDLTMMRGSDGYFAFPFRGTKKIK
MDGSRKKEDPINCIISVTYPNKVGDEWEEGKEREVNFNLERVDDYERDIHVSILCMLHAQ
LDNFEQALGENANSFYFKKGQRVMFLPKKSKLFNRPTVEDSDMFSIIFPPASDQDFADDI
YYRIIVTCS
(SEQ ID NO: 35)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
O13706 (O13706) HYPOTHETICAL 11.8 KD PROTEIN C13F5.07C IN C	36	0.47
Q20960 (Q20960) COSMID F58A6	35	0.61
CAB59514 (CAB59514) HEAT SHOCK PROTEIN 70	34	1.8
Q45851 (Q45851) NEUROTOXIN TYPE F	34	1.8
O17208 (O17208) C01B12.2 PROTEIN	33	3.1
BAA83026 (BAA83026) KIAA1074 PROTEIN	32	4.1

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 1 to 954 of CT1044: this corresponds to nucleotides 143768 to 144721 of the genomic reference sequence.

TaqMan Primer/Probe Sets:
5'start=330
5'stop=350
3'start=406
3'stop=427
5'primer=GCCAGTGAACACGGTTATCGA (residues 330 to 350 of SEQ ID NO: 34)
Tm5=59.57
3'primer=ATCGTTTCCAGTCATCTCCGTC (residues 406 to 427 of SEQ ID NO: 34)
Tm3=59.04
probe1=CTCGAATACGCTGAAGAT (residues 382 to 399 of SEQ ID NO: 34)
probe1start=382
probe1Stop=399
direction1=Forward
Tm1=69.00
score1=1.99
length=98

CT1045
Nucleotide
Genomic coordinates:
Start: 150687
Stop: 154344(SEQ ID NO: 36)

Amino Acid
METTMDNVVQNNDVTKPTPDVATVTTATEKRQSCKEKKDQLKAECPQVLRALKLSNTLKA
NFGKSMSAIFAQHLVDMTNAKHFKDPKTKKILELDGSSSSDSEEEEETSSSSKRKRGSGA
RSASSKKEKCPNTIKNWLNDAQGVFRQFADIIINLPSFDDLRDEVKDEQTELKTIYDLYR
QDMEKVVEEVLGRQDLFDHKSEIAKGLARFDTHVSLLPSDRSAVLDSSISKELEKNSKGP
NSNIFDTLNTLKEEIKELLCHHVKYLLQNLTPEDANFVFNSSVKYVKKSYQYYIQTSEME
SDEFKSLLTGVNIKILEKIISSDNNVATPYKHITNPRNIISSLQKVRETKPVSKDYPFRV
DTARDIVLLPETGGISDLPIKPVTLLQLVSYINALFSLERRNVFTDGFFNAACVLISQCL
TNANLLSNDFPKPIELAANVTRHNLLSMKMLQEGSSSEKKSKKKEKKKDKKKGGGGGDDS
DSETDSSSSSSSSSSSSSSSSSEDEEEEKGEAVEKGKKTKRKTKKKPSKDDDLDTISKLI
LKTGGYFHDTSELGNKIRNLIDKDDFAGVAQYAVTITEMQSTPMNQRLVSSLLDLIMRLK
EQVKYSVDTESTSSTAKSNNALDSAKLTSQQVVTMMVDSGAELARLAAFFFVVVDNTVVN
RHEAFILTSKLLPSNENRGLKTVVESFFKNLTISNKVSTSNEEMMSVMPFEDEQQQQQCP
QHEQQPDLKRVVGEVFLEMGKSIVNSFPSNKSVQLTADAFKQNYSPMGRRINLAAKIKTA
ISIGSNISPNILFSNLPESVGNNTVTGLRLTNLLKNISQSAQANNIIKNANTLVNNTMDQ
QNSAAMSILLFPPTSKETSIFPGNDPSSIKLQDMTTMSNLARGFYSIAEGCIGVVRSREF
DEGGVKAYTLLVDSNTMDMAVNFAAQSLEKSMSEALTNNANMNPSNVLEGGSFVDGALSY
MFEKNGSDCEPTPLAKYTMKDVSNRYLKKFNNDKNTQDLYKNRAERALVEQVTNKPTSVV
HSQLANAMGVAVIGAASIKLMEAEAAESEMRAANYQATSKSTNAINITNTIGMIRNTTHL
CTTIAVSAAADMSKLANNHFMSVLNTANNSHSSRRGDRSSLMLQQQQPTHSAFLEQTRGR
GGGVLGSGTEQTKDHVERMKRDWILNMISPEDKNTTTTTPSNAGRTLGYGSNITGINTIK
QDDKSMMDKLSEMSSFRT
(SEQ ID NO: 37)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
Q9XYZ6 (Q9XYZ6) HYPOTHETICAL 75.5 KD PROTEIN	59	2e-07
O55035 (O55035) PEPTIDYLPROLYL ISOMERASE MATRIN CYP (EC 5.2	59	2e-07
VTA2_XENLA (P18709) VITELLOGENIN A2 PRECURSOR (VTG A2) [CON	57	5e-07
Q07034 (Q07034) RNA BINDING PROTEIN	57	9e-07
NAB3_YEAST (P38996) NUCLEAR POLYADENYLATED RNA-BINDING PROT	57	9e-07
O95367 (O95367) CBF1 INTERACTING COREPRESSOR CIR	57	9e-07

Comments:

TaqMan Primer/Probe Sets:
5'start=1624
5'stop=1646
3'start=1702
3'stop=1720
5'primer=AAAACAGGAGGTTACTTCCACGA (residues 1624 to 1646 of SEQ ID NO: 36)
Tm5=57.88
3'primer=CTGCATATTGGGCTACGCC (residues 1702 to 1720 of SEQ ID NO: 36)
Tm3=57.81
probe1=CACGAGTGAACTCGGCAA (residues 1647 to 1664 of SEQ ID NO: 36)
probe1start=1647
probe1Stop=1664
direction1=Forward
Tm1=69.00
score1=1.99
length=97

CT1046
Nucleotide
Genomic coordinates:
Start: 154556
Stop: 156932(SEQ ID NO: 38)

Amino Acid
MSLVENNTQEEMILETTVEGVVEGAEVAPRGVKRPLPSSSSSSSASDSEDDEGGEQPQTK
PPKKKRNINSGKYWKIETIEPASPEMLSAVNDIDNVSKTIPLIDNSFGVQFKKSVSEEQI
KTLLTETIAVEYGTITNVKYSTFNQLERTGEPLKKKRSNNGNNNYRYWQIRIEAAAAENV
TQAVLDAIVEGNDTVIKAILLPEGEGIGLQFNKSVSSQQAKNIVQAADIEFGQVAHMKCN
LFHKMEKADESSNSSGESPKVKKVRRNKSQPTNSYYTFTMIGDSLQERIDNAIKVIEMSP
VKRPFSNSAAAAEEDTTTTTTTSTGVVNPRGIKDIHFFDSSISKGCFTVRNIVAANGEVP
QEEFVSELYTNLLKVEEKVDHPTFKKLIHDRTMNRHIKAWYCICPYYTTGGVPPAADKVS
AKGIATYRIYEDRTGVFQFDGAHTSTTPAQAAEATGAIHKSMLFQSPGTDIQKFLDAKKA
EGLEPISSGEIVYRSKWSPNDSRATRCFKFYSSSDEKMNIADVLSIVHTDGLFSSVHFRK
DTMEYGVAKSKSKIIPKTIKIKKGGDTFHSEEDIEVPVKFTAITSEELNRECNTKGMNSL
RAHKKRKSNSSTTTTSTTSTSTTANTPKKTKKSASAASDPFAKLTLDYVDSTSFVFYNIS
KEMVQRILAQERVKTLKAVKNEEKMEIVEGEEAQETYRGIVKIKTNAKAYNLANKTSGVL
FPADKVCLKHTLEDLGDVLDFDVVREDNVNKTVASTTTTSSENKASGGDDEETPMEFETD
GEKLLHELLNE
(SEQ ID NO: 39)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
Q45759 (Q45759) CRYSTAL PROTEIN	41	0.023
O97003 (O97003) L1156.7 PROTEIN	41	0.030
O02061 (O02061) B0041.7 PROTEIN	41	0.039
AAD55361 (AAD55361) XNP-1	41	0.039
KI67_HUMAN (P46013) ANTIGEN KI-67	40	0.051
P79065 (P79065) NOC1 PROTEIN	40	0.066

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 1 to 935 of CT1046: this corresponds to nucleotides 155963 to 156897 of the genomic reference sequence.

TaqMan Primer/Probe Sets:
5'start=1338
5'stop=1355
3'start=1419
3'stop=1440
5'primer=TACCCCAGCACAGGCAGC (residues 1338 to 1355 of SEQ ID NO: 38)
Tm5=59.36
3'primer=TGCCTTCTTAGCATCGAGGAAC (residues 1419 to 1440 of SEQ ID NO: 38)
Tm3=59.46
probe1=GAGGCAACTGGTGCTATT (residues 1357 to 1374 of SEQ ID NO: 38)
probe1start=1357
probe1Stop=1374
direction1=Reverse
Tm1=69.01
score1=1.98
length=103

CT1047
Nucleotide
Genomic coordinates:
Start: 159378
Stop: 161256(SEQ ID NO: 40)

Amino Acid
MSCSSSSSCSSSSEEENEVGVEGGGGRIGPTEAKKKILRKRKRSSVKSTSSSSSSSSSSD
DSDSDREEKEGRKLYVDIADTRKPPKVRKLDTPSQTLENDLYMSSSSSSSSSSSDSSSSS
GEEESDDDDDDDYDPDNVHVLGCKKEKSPQDIEAEKEKEEEYEEEFKRMALPSRINTSVD
DCVIPDRILTLFSTLLKKNSFQFSQPVSFLRLVMKQVNEAMNSAFSSMLSSSGMRLVEDS
LGDTSKISSFITPQTDTSNSSSSSTFVNNCTDEDIKKRNIAMGRVAELLSNIAASSNEEN
NFRPVVSLMRGPTCGGSNASNKKLNSNRQTIPQVLNKVIFFREIHSVIALYLSSVCVQRA
MNNDNTNSSGYAEGMVTKILNIIGKIPYNEMSREKFISVGRDALYLYQNVITDMTGPKHN
KRLRIPQQQADFCYIIAMLVNDVPITSDLLLTGKATNLVQFASAMVDPAYRLAVHKMASV
FNSSYSVYKVLDLDHKMLLRANLILSILSARNKCLSERKPRTLTQSVYLFLNHLLRNKLR
SSGLTSEESSLGTAVKLVSQQLMYEGVTRQTIEDGCSMISGNFEDEDGVTLKCLGADVKD
VKTVGLSALLSDRLRKNIRRNVPFY
(SEQ ID NO: 41)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
SR40_YEAST (P32583) SUPPRESSOR PROTEIN SRP40	74	2e-12
NSR1_YEAST (P27476) NUCLEAR LOCALIZATION SEQUENCE BINDING P	63	6e-09
VIT2_CHICK (P02845) VITELLOGENIN II PRECURSOR (MAJOR VITELL	61	3e-08
O95815 (O95815) DENTIN PHOSPHORYN (FRAGMENT)	60	4e-08
VIT_ICHUN (Q91062) VITELLOGENIN PRECURSOR (VTG) [CONTAINS:	59	1e-07
GAR2_SCHPO (P41891) GAR2 PROTEIN	58	2e-07

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 2 to 888 of CT1047: this corresponds to nucleotides 160277 to 161163 of the genomic reference sequence.

CT1048
Nucleotide
Genomic coordinates:
Start: 161717
Stop: 165020(SEQ ID NO: 42)

Amino Acid
MFGSSANNFNGDKKSSSSSSAAASSDDQQLGPLGLSTADFKKVAAILANRTESLYLLPDS
PNFKNVINNPNQISIVPFLGSSKAAESGSANKNENQAENSSKGGSDGKKSSQQNKFNLLN
KVEAEEMAFKRVAELIADTPPSKDNPLRDDPDAIPSRNPWVKLTQKNLEYLFWEAVTIEV
SNDRSIRSGRYLQASEVGENPFLMTISVDIRILQRMALNVVWFFNRFFRMVSGLGVENRA
NSTYVATSDAIAQIWVEMLLKNFISGENVPQALKYLKEHYEHVYNKISKCGRQPSYFVVE
FERVDNTIGFVNSDTEHNGSSYMEYRCFDTIRKNASSGPSGGGKSGVLSSGTFFIDNEMG
NNNSSAAAASAPAVSAGVSPSLSPFSSDGDDDDDDCSGDDVWGKKMIFNTSGDGSGESSG
QNGGGASTYKRFRCGENTASLSQKENVRLMAMPKGNEDKQLLKNIINFLNSALNSVENHV
MCTDENIFDEDQAEHYTSNKELYKAIVCSNPANVYRVMVELFVNLILPRLRNPIVSDIET
VQNLPSNNGSVRTKKMVEHGCTDMRYDIPPYAKGKIRLSAKRACECRKLCKDVRCFDKSR
EANLTPSQKAGREVEEPFPRNHNSHRSNAHDFTFYDKYRARMNKLKKDSKKKVKKIDTFT
TTDDFLLQDRNAFDLLRKCFLSASLHHIFCPDVLMVHRGDSFNINFANNKLECYNERNGI
EEVTSSQTVNAKEALEDITKIKMKRGDDIIDVVKSKGLSLREFSKKVSKIVRRFNEITNQ
LCNNCNVNSSNGDVDFHVFTSVCVYIHNIIPVLEDISIFAELGEELTKLVKECRDVAGED
KTYDDIIRNYEITVKYFKLFNALVKFCHRNYNVAVTSAINRRGYMCMVSNLVGYYCKLSD
NAIQYHESLCSLHSSISYADYYTSRNNNSEDGGGNSSSEKSNADVAKTMASFYDQFDKSE
DSKKNKNKTSNEILIKMFQMDRVLDGMDDDDDEDSDSSSSENEEEEEEEEIVKKPAKKRK
VEDVDSNKKTLPKEPAVKKVKQEEDVEMEEVKEAAAEEEKKEEQEAKEEDATEYDDDTEE
DEKAVASDEDEDDEDSKAIF
(SEQ ID NO: 43)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
BAA83091 (BAA83091) HHNBV-XIA	427	e-118
Q9YTL7 (Q9YTL7) ORF 48	88	3e-16
Q18401 (Q18401) COSMID C33G8	77	7e-13
O35788 (O35788) CYCLIC NUCLEOTIDE-GATED CHANNEL BETA SUBUNI	74	5e-12
O96127 (O96127) PREDICTED SECRETED PROTEIN	73	8e-12
O96229 (O96229) HYPOTHETICAL 78.6 KD PROTEIN	73	1e-11

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 109 to 282 of CT1048: this corresponds to nucleotides 164907 to 165080 of the genomic reference sequence.

CT1049
Nucleotide
Genomic coordinates:
Start: 170115
Stop: 170733(SEQ ID NO: 44)

Amino Acid
MAGIGRRDNRPVLHLDIDPNKEIPYNVPPTPIICEKNPFVFNMQKCSDCAPFPPYPGTEK
PFPPYPGTAVEEEEKQKEIEELLVDQSFPPPFPGNKLRDIPRTYPLEFPEKKEKDFPCVD
TTGHSDIPFIDLEKTPPRSDVRHGYHYLINPNKVGELNHIVGKLTEKQENLNKLVLDVDD
VVINLSSTLKELEKLRAGLCKFSKN
(SEQ ID NO: 45)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
PGCA_BOVIN (P13608) AGGRECAN CORE PROTEIN PRECURSOR (CARTIL	39	0.020
CAB40774 (CAB40774) EXTENSIN-LIKE PROTEIN	37	0.13
AAD45972 (AAD45972) WISKOTT-ALDRICH SYNDROME PROTEIN INTERA	36	0.30
Q22807 (Q22807) SIMILAR TO E. GRACILIS MAJOR MEMBRANE SKELE	35	0.39
O14686 (O14686) ALR	34	0.67
Q28226 (Q28226) MUCIN	34	0.87

CT1050
Nucleotide
Genomic coordinates:
Start: 170831
Stop: 171461(SEQ ID NO: 46)

Amino Acid
MASSSSSPVALSSVASSVMMERDEENTLSLRNRNVNKPTPVSAAWVPVDEEDEDREEMRR
LEDFSSDEEDDDNKSCHCDHSDDDDDDEEDPSCFKGFSAGLCSFVRGFFGFLRKSLTKKQ
VFLLTSAAVAAIFKTRDVAKTEEGAATMEENSTDVITGGDGDSGIAADVVSLASEGEGEN
GSLLESIATTLIKTTIENLVDGGEETTEL
(SEQ ID NO: 47)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
O77320 (O77320) PFC0335C PROTEIN	45	4e-04
CAQC_RAT (P51868) CALSEQUESTRIN, CARDIAC MUSCLE ISOFORM PRE	43	0.001
O49209 (O49209) PUTATIVE HISTONE DEACETYLASE	43	0.001
Q9YPA9 (Q9YPA9) HYPOTHETICAL 45.2 KD PROTEIN	43	0.002
Q98148 (Q98148) ORF73 HOMOLOG	43	0.002
O40947 (O40947) ORF 73	43	0.002

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 1 to 637 of CT1050: this corresponds to nucleotides 170864 to 171500 of the genomic reference sequence.

CT1052
Nucleotide
Genomic coordinates:
Start: 173177
Stop: 175862 (SEQ ID NO: 48)

Amino Acid
MTRHGVLVPK GRSRHVILGN VDYTFCTTDN NCVSLDIDFK DNITDQNIQL
LNKKLGKKTA KKIKKEDAPE TKENSDEDIY ATKEFEQTIK GLQTKKGATE
ENAIAAAAAA ATAAAVEKAM LSESEGKSMV INRARMVLSK RDTSQKQFTA
LKNRESFFSV LIFETGSVIV VGLQDPSLTK LCVIKATTDI ADILQKNISV
ANVSIVNTVS TFNRFHLNFI RLGKFFERNC ISYSYNPETF PGMFFKLRVP
AKPLLPGETI GEYYTKVAMM RDSKDPNFKM SDWLRIKTAL TFKVGKITVL
GEGESGCGDV SVVSKLLFGL FHYFMDNNIK MSPKEAQRVR EKYGIPHLEW
YLYIDMLLHS YPYVKPSAEQ VKRAMVDQQH ISEVDRTYYG TKNSMDAAMS
ANLVPSKEES ISFIKKIRSQ QLFGHLCKPS KETTRRAIDT LSFDPINQDR
WWNKNDQYYG KERCDPFSVA RLVSVSENTN SMMNSRISCQ GKWWLDENEY
KDKLDHIVDL CTEEIVEECE SKGFIASPFL RKHQKEKIPT PYVLLARACN
QKNGNKMSIN NNSNYLSGSS RAKRNAKLQE KHRVTLARLN TMMASYRFLN
NYISTDIAPD FAKLFGNDVY SLLHLMTNLP KSRGHALTYN ERALSSNEST
YKTPGNAYFS TLFEKSIINN QETANKGNNR KRKFSRIGQE KSSFLCNACG
VNLNKGSDEI IKGICTSCDQ NSTSYIENAL SDINRDKKIK RFKAAATHPP
VKQELVDSLS SSSSPSSSSS QTSNKNNRCT PSDFIDYVYK FTDETTGAPK
VGLVFKMCDI LASLASRRGM EDRPTANYRT SLHSATQNKT NLNKLLVSAI
KETGATETEA QIFNKIIGSE KGLSILCQLV ERRNKDNNVF D
(SEQ ID NO: 49)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
gi\|6647869\|sp\|O29874\|TF2D_ARCFU TATA-BOX BINDING PROTEIN (TATA-...	44	0.001
gi\|6647868\|sp\|O27664\|TF2D_METTH TATA-BOX BINDING PROTEIN (TATA-...	43	0.002
gi\|3122925\|sp\|Q12731\|TF2D_EMENI TRANSCRIPTION INITIATION FACTOR...	43	0.003
gi\|135643\|sp\|P13393\|TF2D_YEAST TRANSCRIPTION INITIATION FACTOR ...	41	0.010
gi\|135627\|sp\|P28148\|TF22_ARATH TRANSCRIPTION INITIATION FACTOR ...	39	0.038
gi\|135626\|sp\|P28147\|TF21_ARATH TRANSCRIPTION INITIATION FACTOR ...	39	0.050
gi\|3334374\|sp\|O43133\|TF2D_CANAL TRANSCRIPTION INITIATION FACTOR...	38	0.065
gi\|135639\|sp\|P17871\|TF2D_SCHPO TRANSCRIPTION INITIATION FACTOR ...	38	0.11
gi\|2833518\|sp\|Q57930\|TF2D_METJA TATA-BOX BINDING PROTEIN (TATA-...	38	0.11
gi\|417896\|sp\|P32085\|TF2D_CAEEL TRANSCRIPTION INITIATION FACTOR ...	37	0.15
gi\|417882\|sp\|Q02879\|TF22_WHEAT TRANSCRIPTION INITIATION FACTOR ...	37	0.19
gi\|121568\|sp\|P22010\|GR78_KLULA 78 KD GLUCOSE-REGULATED PROTEIN ...	36	0.25
gi\|3122941\|sp\|P93348\|TF2D_TOBAC TRANSCRIPTION INITIATION FACTOR...	36	0.25
gi\|3915894\|sp\|P52653\|TF2D_ENTHI TRANSCRIPTION INITIATION FACTOR...	36	0.33
gi\|1729908\|sp\|P50159\|TF22_MAIZE TRANSCRIPTION INITIATION FACTOR...	36	0.33
gi\|1351224\|sp\|P48511\|TF2D_MESCR TRANSCRIPTION INITIATION FACTOR...	36	0.33
gi\|1729907\|sp\|P50158\|TF21_MAIZE TRANSCRIPTION INITIATION FACTOR...	36	0.33
gi\|135640\|sp\|P26357\|TF2D_SOLTU TRANSCRIPTION INITIATION FACTOR ...	36	0.43
gi\|1709903\|sp\|P54637\|PTP3_DICDI PROTEIN-TYROSINE PHOSPHATASE 3 ...	36	0.43
gi\|2833459\|sp\|Q55031\|TF2D_SULSH TATA-BOX BINDING PROTEIN (TATA-...	36	0.43
gi\|586175\|sp\|P32623\|UTR2_YEAST UTR2 PROTEIN (UNKNOWN TRANSCRIPT...	35	0.56
gi\|2833446\|sp\|Q52366\|TF2D_PYRKO TATA-BOX BINDING PROTEIN (TATA-...	35	0.56
gi\|3915739\|sp\|P18428\|LBP_HUMAN LIPOPOLYSACCHARIDE-BINDING PROTE...	35	0.56
gi\|135634\|sp\|P26354\|TF2D_ACACA TRANSCRIPTION INITIATION FACTOR ...	35	0.74
gi\|135636\|sp\|P20227\|TF2D_DROME TRANSCRIPTION INITIATION FACTOR ...	35	0.74
gi\|417102\|sp\|P32103\|H1_EUPEU HISTONE H1, MACRONUCLEAR	35	0.74
gi\|2833477\|sp\|Q57050\|TF2D_PYRFU TATA-BOX BINDING PROTEIN (TATA-...	35	0.74
gi\|3041729\|sp\|Q03410\|SCP1_RAT SYNAPTONEMAL COMPLEX PROTEIN 1 (S...	35	0.74

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gi|3122946|sp|Q42808|TF2D_SOYBN TRANSCRIPTION INITIATION FACTOR...    35  0.74
gi|126745|sp|P14873|MAPB_MOUSE MICROTUBULE-ASSOCIATED PROTEIN 1...    35  0.74
gi|4033393|sp|P78695|GR78_NEUCR 78 KDA GLUCOSE-REGULATED PROTEI...    35  0.74
gi|126511|sp|P12744|LUXB_PHOPO ALKANAL MONOOXYGENASE BETA CHAIN...    34  0.97

Comments:

TaqMan Primer/Probe Sets:
5'start=1268
5'stop=1291
3'start=1327
3'stop=1350
5'primer=TTGGACATTTGTGTAAACCTTCAA(residues 1268 to 1291 of SEQ ID NO: 48)
Tm5=57.29
3'primer=CCTGTCTTGGTTTATAGGATCGAA (residues 1327 to 1350 of SEQ ID NO: 48)
38)Tm3=57.45
primerScore=0.74
allele1=
probe1=AACTACTCGACGTGCTAT (residues 1296 to 1313 of SEQ ID NO: 48)
probe1start=1296
probe1Stop=1313
direction1=Reverse
Tm1=69.02
score1=1.97
length=83
```

CT1053
Nucleotide
Genomic coordinates:
Start: 175839
Stop: 177107(SEQ ID NO: 50)

Amino Acid
MSSTDLSKNAFHDWVVSKTDCEVFDVHCETDRDCGAACENTYSVDGKEVTKFSCNQQSGR
CARSVYSASSLERAANDLGHIIGIIKKNPKLEEELPESFLWFINHNGGDLFVNKRAAYYD
TMHLSIGKLDNVDTLAQGLDKRMASSLREHLLRKLDSILLQIDKVKYEKAKKWILDITQE
AGTEEDNKEEEDAKKEDQSLSVSEIVDVLTGTHDPMPLRARGFIQKKIYPLSRNELRELA
LKELFPEETTSPQVLSRQHDVSTREDLCNESMNAGRAESIFSDPDSGEYVATCACLYSEY
LTGPACKHKTYRYVIDYDKWKRTGRPEFLTDPVLHFKKAEAVCKSTNPNLRAIYSPDNKG
FLCAPVAELVKTALTFRGSHEPSLIVERDINQAENLPSNSFGVNWPYVNLLNRIQDQYT
(SEQ ID NO: 51)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
Q26648 (Q26648) TEKTIN B1	37	0.30
RRPP_VSVSJ (P03520) RNA POLYMERASE ALPHA SUBUNIT (EC 2.7.7.	36	0.52
RBB1_HUMAN (P29374) RETINOBLASTOMA BINDING PROTEIN 1 (RBBP-	36	0.68
CENE_HUMAN (Q02224) CENTROMERIC PROTEIN E (CENP-E PROTEIN)	35	0.89
RRPP_VSVIM (P04880) RNA POLYMERASE ALPHA SUBUNIT (EC 2.7.7.	35	1.2
Q89487 (Q89487) PHOSPHOPROTEIN	35	1.2

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 1 to 1109 of CT1053: this corresponds to nucleotides 175933 to 177041 of the genomic reference sequence.

CT1054
Nucleotide
Genomic coordinates:
Start: 177123
Stop: 178524(SEQ ID NO: 52)

Amino Acid
MSASLILDEYLKKTASAVLDVADSFEKIKGEIQSPEEAAALSVALYGAPPKPSASAVASII
TGERTSLNDKYLSDNVLLKMSVARVGQENNRKRADQAADEIRTIMEDITGSLSGAYRQYSP
LEEENKVHIGIMNNKTPSIVCGYYTMDTSISSEPLSLTDFQNPTVIANVTKRMESIFSKVD
SARSTRFDAFVNGVANNMDIKSSIDWANMVENVIKLPDSTPNPCSVDTIVSRDASVVKTAV
NDIYASVGKSYCRPATQLTFMSEIEKLRKAAVVCFEALMSDTRERAFVEFLFYVSFKEDAS
NTNSKLFVQNKLSSMSGNPRQPIKLVRRSAEETLFGLCFMFKVMPPEFMNCIFNFPTIPHS
TQYHGLYGTCLTPLLRKYGSSFEKSWAHFEEILSERANAVKKFGVNDTRIDCLDAVANLTG
PVYVLILDLVRTLSAQRSCSTKFLREIKENYLLWNRFVSX
(SEQ ID NO: 53)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
gi\|126194\|sp\|P17279\|LEU2_RHIRA 3-ISOPROPYLMALATE DEHYDRATASE (I...	33	1.4
gi\|6685598\|sp\|O95613\|KEND_HUMAN KENDRIN (KIAA0402)	33	1.4
gi\|2497227\|sp\|Q04893\|YM96_YEAST HYPOTHETICAL 113.1 KD PROTEIN I...	33	1.4
gi\|134393\|sp\|P17065\|SEC2_YEAST PROTEIN TRANSPORT PROTEIN SEC2	32	2.4
gi\|547908\|sp\|Q02455\|MLP1_YEAST MYOSIN-LIKE PROTEIN MLP1	32	2.4
gi\|2496893\|sp\|Q09462\|YQ52_CAEEL HYPOTHETICAL 30.9 KD PROTEIN C1...	31	4.2

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 1 to 899 of CT1054: this corresponds to nucleotides 177561 to 178459 of the genomic reference sequence.

TaqMan Primer/Probe Sets:
5'start=678
5'stop=701
3'start=754
3'stop=777
5'primer=CACCTAACCCTTGTTCAGTTGACA (residues 678 to 701 of SEQ ID NO: 52)
Tm5=59.08
3'primer=CAATAAGATTTTCCAACAGAAGCG (residues 754 to 777 of SEQ ID NO: 52)
Tm3=58.08
probe1=TATTGTGTCCAGAGACGC (residues 703 to 720 of SEQ ID NO: 52)
probe1start=703
probe1Stop=720
direction1=Forward
Tm1=68.92
score1=1.92
length=100

CT1055
Nucleotide
Genomic coordinates:
Start: 178529
Stop: 179348(SEQ ID NO: 54)

Amino Acid
MAQTSKMGTNKRCFEEEVEEERQQPFTKKSKSEPPSFEDKSSSTSSKKKSKSNKHTKTKE
EQLLEFVKDLERSDPTVPDEKVKQEVEEKSPEAIAEIFSMFGIAQDSKFKSLLPIERIKS
ITTKIVIDAINQPVRKMLVDHLYHFKEMQNVVEKYKDDSDEKLSVILKSKKSPKEFDLSF
SDYVDRLNRILVGVIKRVAGAIESKELLQSNSMIMNSVLGTVVSNIPYNMKINICVFLTN
FICTFANDDLYTFFRDDEKFVMSQVTRYISKD
(SEQ ID NO: 55)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
O01761 (O01761) C. ELEGANS UNC-89 (GB:U33058) (NID:G1160355	45	8e-04
Q17362 (Q17362) UNC-89	45	8e-04
Q17595 (Q17595) SIMILARITY TO MYOSIN HEAVY CHAIN	43	0.003
O31329 (O31329) ERPM	42	0.004
FKB3_YEAST (P38911) FK506-BINDING NUCLEAR PROTEIN (PEPTIDYL	41	0.007
AAD55361 (AAD55361) XNP-1	41	0.009

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 1 to 661 of CT1055: this corresponds to nucleotides 178612 to 179272 of the genomic reference sequence. Hit to public sequence gi|6856160|gb|AF173992.1 to CT nucleotides 647 to 819 of nucleotides 910 to 738 of the public sequence with a 100% homology, a score of 343 and an Evalue of 6e-97.

TaqMan Primer/Probe Sets:
5'start=269
5'stop=289
3'start=340
3'stop=360
5'primer=CCCCTGAAGCTATTGCTGAAA (residues 269 to 289 of SEQ ID NO: 54)
Tm5=58.07
3'primer=GCTCTTTATGCGTTCAATGGG (residues 340 to 360 of SEQ ID NO: 54)
Tm3=58.32
probe1=AAGTTCAAGAGCCTTCTT (residues 322 to 339 of SEQ ID NO: 54)
probe1start=322
probe1Stop=339
direction1=Forward
Tm1=69.00
score1=1.88
length=92

CT1056
Nucleotide
Genomic coordinates:
Start: 185432
Stop: 186830(SEQ ID NO: 56)

Amino Acid
MAVGDYLSMSSVGEATLVGFMILNFINFVTILSLIIYAVTDVYRRCKRPSTNGYSGCTTN
VVSSTLQEANLVTTEKDKPVQFVRGLVPRKMMEKYRSDLSPKNVGEYILPSEKETDKLKS
DYKKGKKVGLLTALSNGHDSNKRIIGPRDLISRDDVKDKSYVFKRLSKDPLVYYSSATSK
YVRKFSPFRAKKFMTSTQLGSKLVYPHPIRYGTAFVLPTGYVINKAYGMDNEDLHTWNPP
SSSVLVPDSNNDRLTVECAKTDPTHRIGIYGFGGSDDNRRAKEEGYVEMLLCNCDNHKDL
LKAPLITEYSTNPTEIQVDVAAKRVLFPAPGSEPVKSSQVTSAAHQLDGATGEHDISHEP
VKLSDTGDYAVGSPIVFKPVYGTSLVNLPETGSPLALNCPCTDKADGIYQVNQKGGILYR
DMVGYLNANPVEAASLSSSDSSSWLTTGNKISSVTCEGEKIKKIV
(SEQ ID NO: 57)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
Q99175 (Q99175) HYPOTHETICAL 58.5 KD PROTEIN	34	2.2
CAB49723 (CAB49723) HYPOTHETICAL 52.6 KD PROTEIN	34	2.9
Q9Y6X0 (Q9Y6X0) SET-BINDING PROTEIN (SEB)	34	2.9
Q9ZXH3 (Q9ZXH3) INT44	33	3.8
Q55105 (Q55105) MULTIPLE LIGAND-BINDING PROTEIN 1 PRECURSOR	33	5.0
Q9WXH8 (Q9WXH8) PYRUVATE ORTHOPHOSPHATE DIKINASE	33	5.0

Comments:

TaqMan Primer/Probe Sets:
5'start=663
5'stop=684
3'start=705
3'stop=725
5'primer=CGTGATCAACAAAGCATACGGA (residues 663 to 684 of SEQ ID NO: 56)
Tm5=59.59
3'primer=GAAGAGGGTGGGTTCCAAGTG (residues 705 to 725 of SEQ ID NO: 56)
Tm3=59.41
probe1=GGATAATGAGGATCTACA (residues 687 to 704 of SEQ ID NO: 56)
probe1start=687
probe1Stop=704
direction1=Reverse
Tm1=68.99
score1=1.88
length=63

CT1057
Nucleotide
Genomic coordinates:
Start: 190875
Stop: 193236(SEQ ID NO: 58)

Amino Acid
MEYMEEGDIAERRSEGVDYILDENSACVVNVKSIRNRLGAMDAEEAQYAQDISAQLVTHI
IRLAHCSESNKIKDTIASIAGLFINNIFDNNSTKNKLKTYNQFKAESQNKSSVLNIFGSL
DPLSMLSSFMGSDPAKSGGENLDKSLGVLFEVLQNYNPCKIDDIVLLEMCPSKCAACTGL
KEAIRQEQPMEAMLLFFKCINHNRFNFGSDIKSAYASETCMRYSQDERAVVVPLRSILLG
CLDRDDPAHTLSSFGDTIEYADSDNAWVSSLFAAVSRMPMVDRAVIAHFYVYTMLSRHRR
VSGDSFKQFVYTVFVRMIYSAIEILFCDTENSSVECDGKHFLSYVNAMVNVSVLGSTFNV
LKAYRSWVVDQASVAPVLDIISGGWKKNYPSPDHIKRVAYDISQVINHLASPSRMVKGNN
KASNVTSGLDSIRSVRQAEKYIPFGILENKAGYGVINIAKHNISRPAREQSNGRNFNCNA
LHILPSIKGCEALGAQKGSADQTVNVFDNFVASHMDIAMKKQGSGKILGLLTSMIDRQGL
TTSFPSSEAEYKKRIHDFTRYVIFSSTPINDELVNSRCILPHSNVLNSPISLRNIDPESV
PDTRFHFLLMMWQRPNIDEPNLSALTTSQLELLLSKNQKWDKLTTRAFFNIDRINFQMAD
AIIKNVSGSGFLDGSKTASSSSSAPNFFQIFSGAECTAKQLQSIRKFIGESMQHVQKEWS
SAVNNGNRGVENYDGLNAQFSEELFELLYKLIIEEDMRPSSLIASSEFLSNYVNAMDELL
IRANAS
(SEQ ID NO: 59)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
CAB52133 (CAB52133) RCOP C7 (FRAGMENT)	34	3.0
IDHC_SOLTU (P50217) ISOCITRATE DEHYDROGENASE [NADP] (EC 1.1	34	5.1
Q23615 (Q23615) ZK822.4 PROTEIN	34	5.1
YSW1_CAEEL (Q10017) HYPOTHETICAL 63.8 KD PROTEIN T25D10.1 I	33	8.8

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 1 to 636 of CT1057: this corresponds to nucleotides 192639 to 193274 of the genomic reference sequence.

TaqMan Primer/Probe Sets:
5'start=1214
5'stop=1236
3'start=1281
3'stop=1303
5'primer=TCATCAATCATCTTGCATCACCT (residues 1214 to 1236 of SEQ ID NO: 58)
Tm5=58.13
3'primer=CAGACCTGATACTATCCAGGCCA (residues 1281 to 1303 of SEQ ID NO: 58)
Tm3=59.10
probe1=AGGCTAGCAACGTTACAT (residues 1262 to 1279 of SEQ ID NO: 58)
probe1start=1262
probe1Stop=1279
direction1=Forward
Tm1=69.01
score1=1.98
length=90

CT1058
Nucleotide
Genomic coordinates:
Start: 209615
Stop: 227849(SEQ ID NO: 60)

Amino Acid
MDQYPEVRDTPQTEQEQAAAQQQQAATTTAAAAAAAAPTQYSNTVSAETLSAISEDGKLE
RSIAASCWINNLNPDEKMAQRVQFHPLSSTTTYDSENVNPGSSVVFLKPRALPTGGTCLA
PNYIAVPTLRAASEIIDSIASTSLYQCSMFNSWNLIPIFMSNSKHSQFGDRVIKRSMIRN
CFSKQKNVENLLKELRRRKVNAAKAFSHAVQQKSAVNTALAAWNAGSAANLEKLVDFCKL
KYSPDRKYKAGGLFSASATAQSQSGTSSSSVEHTSNDFLLDILKRHKGTSLDLDSATNTF
DTALSRVFTEFKEQARAAVDAAADSDHLSASDPIFSIVRHNSRREGILDSVPNIGMLAPR
SKYSVAEYLMADRDESADIAAKIGTKIATDFEALRGDNNKRRADTSVDDLKESLADSIEK
TSIKNTGDINSVTNIPTDTEEYEFSLHITQLFAQAFLETMGSLLSCAFGVQFPFSDEGFA
AIERIIRKTDPDTGKVSEMDPSSLSDQYLLLVGNFQVSPFHVSDPKDIVFGRQVTPNTPI
LSIITRSKNDKNETSTIINFRDRLLVNDTVLRDATQNVSTSTPSQRRVPTAAGEPKKPML
SGCLPIIRGPQVVTRESDDMISGLVGDWYISLGVYYAMGSSAAAIAAGHQRALASAESIN
SPMMKKFSKKGGKYTEEEKRIKKAMRRNADRSARILALLGQTDAQYGYVEHNSTLDSFWS
SNAAIRAKAKEDALSRAEILAVRKQLDGKCSSSRDEYSMVERYLRDSFFRSVNRSGGGYE
MFDQGFDMGRFADFLSDNSAARNAWQQYAEVMRGLSKHEKRVFNIEGLFSALNSFKFPLV
PEQGRKKTVGGRHRLNNLKAANKIINGITEMTLQSAIDGTGISDIIGSVSDGWGNTTAQP
SRVKALKTLSNFSGNGNVVSIPVSRAVKCAAGSRGGETLKCVDIPSVIIANLISDKRILD
QLCGGGMNLAHEITNFIETIAGKEHTGKESVFLSPRLSVILLRYIWFNAAVVSLTDSNIK
MPLNTMSEGTGDDIYRDYLAIRGMVNNYNSSLSSISVKAISDRYNCGSGNTSTSNKNVTI
KTQGELLTVLQQTANALSAFTNKGGVGATPDAANMANVISPIANADVVKNTNVVVSGLDR
ITETINFFSFLSQIKTMNENIEEYLRRYRLGEGLDKKELDNFVYPNIAAIVKRELGVSGS
ALSSNLDTDRPITIDLNTEQPLIVKASKGYASNRYAKLFNKTTRTAAEQAQMEQYNAQMA
ANTIPQLVNRLTIPGSITADTAINVVKAFTENGEFSNAETHLGVMGNAINEMQPLFTDGF
NVANKRLTVNVGSVSKLIQNGLTVSLILAHSKASPYVFKPLVQDFAKLLLAVTAETSLVV
SRSQKSFFPIPPSVFSSGGLFKIDREMFDNMKTDYVVEVIRQLSKNATAAIERCNDSDSA
ARIAKSGEIYNKDVASTTAAPGTSSSALTLFANNLQNPAKVWSMGALPHFDMAVVPKLHG
ISHDQMFRLSTYYQGIHKMELNSDCKPEEWDNSLPGNRASKFFGLSSVSDNNRSFNLALD
TLLASPAEICDLVTREMVKTSNDIVHNIGSNSNTDALQKSLQVGASAVEKYDESTLSTKE
TDVYSLVSALAKSKSPLSSSSSLSSEGHLTSKEIDRTWNTPALLGTAKTTSYSVSEDALN
APLSAVLDFRRNVVDATKSLYEVAAVCSVMSKEEDVRSSSRKIMGMVEQESPVMQDIGID
RIASLVSTVATPKQHRRFLQTVNDYKNYLIRKVASNPLLSSRLGGISPTSGNTDYNLKAV
YDGVVSSSSSMTPSSMSVSDRFWSGVFSQCLETGPSMFADAGHGGSNMFQITAPKLYGSR
VNTYAALSSGVERLRDSISSATQERKNRIAKSIEALETFVTDVVGGDTLDQLRKAQNMYN
KLSDITSNSIYSDFGNIDCAKIMKNVTSKKMTARQQSDTILSSLLHELAGLVHKQQPQLA
TQFALASHVIKAKYVTNDLNNIHEKETFSQLMAVAGVADYYNVSAAAMCQRLVASDVTMF
LGGTMLQQGLFVSFLLNNVLFSQVSDNIKMNELNDETKSLLVKLVGFCGTVSDALGSRHV
SSIRRVQNEEDKKLDRSFVTSLYSAYRDLRKKTELYRETDTINKLFGHQNFMSYESSMLK
RTSLVHDAVSGPRPRRYSTLEDVLEAPSTVHKSFMVSYPERAAASRRVKRAGLRALADNR
MESLYGEEVLNDMRSSAVSSEMMDIEYGEGGFMMMISDDEDDIAFIDSEEESESSTDFSS
SDEYSDSSDEYDFDDDNNGQSPYSTTSYSYDALDRLNSAAKPLTAIYGCRGEGEDDEEND
LYEEEQERRRRRSSKMGKILRDLHESDDDDDDYFDDEFDGERSMSETIATRRAGRIQYGP
GFLSHSNILNRPAKARAFLTRGKKFRPSAYDRFFMEDDDSLLFSDESTTSSSSSDSPFSS
FSKGRKCKRRTSEDQCAFVKRVVRAFVPTRVTMINGRVSMITPVTSENTVGFYENYQKAN
KRERARLIEEYKIVKGASATLPDEYVEGRASKQVSPRELRRSLIKAAAYVARTQESNLNI
IFDALTTTSNATLVNDPSTLLGDTLLFAKQLEAITERRNRLMKDLTEISPSLFTSFGDAS
KDTQMMADAKQIVSGGNFKSAGYLGVPLRTLASCIKGTNTVDRLLATKNKNHLEWMTTAA
IVFARSFNDTTFHALEDTLKMTSALTDMYSAFTNLVGSEHSQRLKVKSTLLDSIFNTRMA
HTEAVMGLVYPTAFINHEMPSDYTQRREMQSLALNILRGVNCSQLPRKDIGDTAGLLTFI
TSRKFAGYGGERGGLSLYRMSIVDALSCPSDNRLKGAVSLEVGKWQDMGEEIFYKRSNDL
VDFCSKNNISLENAVGPIARFVPNGTNMADIGMTDIISRTVKDDASMIRLRRAEEGAGAA
GKFITASAMGNLYGGIDTVVNLTEKLYDSFVLLQDSDSFNTPTEMATAIINRMKSRKHKA
LKTPFGGDIATYKNFPSSSEAIVVRAKEMRNSISTIVMDISKSRGINSFSSRSGSTLAKI
STSEFERILETSAVLSNTKANLRTIENRLAEHYNKLKQFSHISNDGLSETRAVVAVIAES
LTPVYADDTSERGASVSELLTDNTLLKFIVQNELKNIEEAKRHVTAAIEGSSQLHEKMLS
LLVASADINRMSAQNNLECKKLTEGNSNFVPMTNDQGGTFIKHKETGIWLKTDEENNTSS
IKDNDQRRVAKTILAIVEDNRNATIRSRLQSLCFGKYAMNDIFALDDADIKNMDKLIEKL

FIGURE 3, Sheet 34 of 160

GEALAEKASPSSSAISSSSSSNTTSSSSSPSSSPSSSSSSFSMDYSNNLAKTIPYMPIVF
QNKQSNVNSSDASSSSPSSSSSSSANIDNVEHKKVALQQLQTQESNDLSNVLSVTTKHRF
ASHNQAATVGIFNGRQHAETVVAIPNANKANNNATVSAGQGILTRFSAPENVSSTSMQLP
PSSSSSSNGDDNKVPVTVRLNQYANSILSSIENASEFKDLKEAERKIDLAIQAASTTETK
EMVTVSKCPSANQTAITAISQAKSLKKSALELLERVIKAVEVYTPDSSIAAVSLPVNGDS
MVSSSSGSGSAPSSSSSSSSSSSSSNVTDYFNYAYGKLKNIDENTEEGAETVQKNMVEQD
AAVRIPLLVSYAPFSEMMRRAIDKLNEYYQLIDAIKTKIVSDTKQASSWAIKETDKELDM
DKEQVISKINNLQQNFSNESDKIKMAISVLDNKRNELELQNNKTRSFIETTKSRIEAGGG
DVANFKEIIDYENTSENDNNLFQSLKAFAADNSGTVYTPTDMSNGRDTKSDSKFVDMYNK
QILEGGIKLINEGQNTVKVDFSKALEAFPRQSNGASEPVSSSVVERRQRERLQAVEMFMA
IMMERTESLRKRLADSAAQWNTVNNVEETVNSGMVNIKSERLTEIRNQAQIAESTALNSI
NDEIVESPLTLSLGARVDQLLIKVDRVGSIQQQQQQQQQQQQLPKLTATEQRKEQQYAAD
RVVYDPSYTCFLQPLHETIKRISSVYNSKNKGPLSNTRGVPTSDADLQLMTITDLSRSVL
DSSSTSSKKMLYENVPSSIVPGLCQQCAMMITNVHEATHTSPHSFNFENKRSLKQLTEML
NAATSSSDGPAVRHDVLTMLESNNGYVKDFGFTHRQKVACITPVNTLLGGTFSGNVAPNT
VILPTSELFNCPGVENDKFRSMVNRTTDKNVADAPKSSASIVETLARTSPNAEHLYFPFK
DQRRHFNSITDAIISGMSGESSSQLNTTCDQNLVNIDQTTGFPVFTGRKQGERRIVHTEN
TMEGARKDKNSGIPSCTKDRQTYIDMGTKFMVAPGSLLNANKEETLRLNRLSDINNVRHY
GTDVHVAGANSAWRIGEVVRAASSFPDGDKESAMKKMLLLGSVSAISAQKSASHINDPTA
LLSTNTSIQNLVKEAFPDPVCSSNYLGSAESTFATQLAYRQRLFPNGDDENVTTVSNICP
MDLMGSTKRYNDAFNNIFGSKMTSTNKKGSNCENLLKSAMSNVPAINTAFGAFEEASSSV
RNRLSPLYEDSTKYSSNQLAVQAMTDTAVDALSAVSTVVGRQNGRNTLLSLPTSITSIAT
SGRPSLSYSSDMKSNLIKTISRINRDASLLSMGDSQVAAGSSFFNSFLRSSSIPVTTSQD
GNVAAAEIVLGTILDKTVEINKRFEMLGGGKMVAGSPEARAIQRNTMSSILQMNENELAR
DLCEIENKIETRQLRDAFQDLKRSMLMTPGGVGAISSGASTNNVPLSLLMSRVDASSGLL
MNNNSANVMEAVDSFNTTPLLVRHMMLDSGKSPVPMAKEIRSMLTQPRALTARALLSESS
PLLTEICLYNTRDTQPERAVDRLLTSAYLVKQAKRFDGVDPAFPAALTCASHLMLSSMDS
HTKSSFMDNIKLHMTDTQCFFKNIERFEKFLGRYGDEYAMSHKQNCNCPFHLHHTFTPSD
NEHLVSSFAFARPEVSMEEIRATPYQANKLISDKHYVMNMSKIDSRVTGSSLLKKVSEWT
EMRMNSNFNGTFEPSRLALSNSGMTTAGVNLDVIVKPNNARSVLGILECHRQHVCTADAK
GTVASAMPAVFQATDGNGNESELIQNALPRNRYIQKSTMNAQTVVFANVLEQLIADLGKV
IVNELAGTIAESVPESVYENTKEMIDRLGSDDLFKSNNNGGVESMDYEDSETTSNNGPVL
ISEAMKNAVYHTLISGKAARPENVPFASCASGPLAFDFLLSKGDTFEEKNAEQGAAAAVS
STYSSSSNTTLRKHLARVFEAISKQVTDAEFKDILNDIERNISSDYTNCPPNTNQNAFAL
AIKREFSRIVSFLTILRKNITPALVDPKGALHEKVAIYLTLLSTKSKLENFFQYGLSNSS
SVDLSHLKPINCSNNVKNIEDTFMYRNVHPILIMALPENFTALLQQEQMDPDTAIESRRS
LTTFLNHPNTASMANGARAAVGAGGGNPMGLYLSSHILHESTVTTSNPVTDTTENVNYHS
SVTQDPVMVVNPFKDSARLIVNNNNTGIDVLNDKSCNYLQVSMPSESSGLVTNTGCSSSS
SSSSSDTFKYVRRDNTPVNLPRVTPAVLCSDASSNLLDVFSRADIVLENMNVRFGFMPEI
IAAVSKFKGLTKEEVIKQMVSQNNINNNSNNNNGNGKKTTVDPVTGDIVITNATFPDTRP
LYTAANGGTSSFKWGDINDRKMHAKAFPTFFIGNPTAAATANGVPLTSEGISLTEEKRKK
IAGISEGSIGTGALRAAANTRLSSDMEPVMKGWNNIVQLQQTFKKASDKLTHLLRSGGIP
PRSQETNAIINKMHDSFKTLEECRRVIQDEAALLVATSDLLTGGYGGDAALAMVSPVRPE
MTGLIGAISAPVRGISHLLKLGGVSAANAAIRKRLNLPTSNGKTLPEHGIVHKSAKTLLL
DSDSISNLYNTDLQDVVSNARDNNNLGRIMQSLGLKGNNAGDLVYSARQLTDLITVPEYG
NNRDLTKRQAILKMLISNPEILENVADTIYLTTGKNALAPVSAQEMACASLTVGGSGGGK
LSSDDNVQSLNRLYFRV
(SEQ ID NO: 61)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
SR40_YEAST (P32583) SUPPRESSOR PROTEIN SRP40	80	5e-13
O94317 (O94317) SERINE-RICH PROTEIN	80	5e-13
O95815 (O95815) DENTIN PHOSPHORYN (FRAGMENT)	80	6e-13
YM96_YEAST (Q04893) HYPOTHETICAL 113.1 KD PROTEIN IN PRE5-F	76	9e-12
AGA1_YEAST (P32323) A-AGGLUTININ ATTACHMENT SUBUNIT PRECURS	73	8e-11
Q9Y076 (Q9Y076) PROTEOPHOSPHOGLYCAN PRECURSOR (FRAGMENT)	71	3e-10

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 1 to 704 of CT1058: this corresponds to nucleotides 227240 to 227943 of the genomic reference sequence.

TaqMan Primer/Probe Sets:
5'start=8829
5'stop=8848
3'start=8894
3'stop=8917
5'primer=CATTACAGCCTCAGCCATGG (residues 8829 to 8848 of SEQ ID NO: 60)
Tm5=57.78
3'primer=GCAGAACGAACGAGTCGTATAGTT (residues 8894 to 8917 of SEQ ID NO: 60)
Tm3=57.76
probe1=GAGGTATTGATACCGTTG (residues 8861 to 8878 of SEQ ID NO: 60)
probe1start=8861
probe1Stop=8878
direction1=Reverse
Tm1=69.00
score1=1.99
length=89

CT1059
Nucleotide
Genomic coordinates:
Start: 228374
Stop: 230564(SEQ ID NO: 62)

Amino Acid
MDKVCVISNTRERTFKVPADLLCVATEPEISTKEEDAGIEIETRVVVFSRCVSVQELHTI
NPNDEGFSVQLFKDYLKLQSAQGKKPIGLYIQIKAGEDLERRLISGGTAYLDPATHLFYL
DFSLYPNYSIFNDISSRLKIIDEDTYNGVVFSNSEEKEKDALVLIRVTFSTHEKAIEAAI
KKIMLRKVFFKDGDLDFGYLRIPKSKLDKFTPYFRSQYGIVNVEKNIPGYIWGEIMKQRV
RCSRWYLYNTDSEWEYKNVAEERVGPRQLVKKYGAKCENLCFRDIDLRKKEAKEKRDIER
ETESRYVVVTLTHKHEMPENMPYFGPKCSVVRLDETRILLCFVDEISYNDEDVDEILSEN
RSLRNVSIRHKENVPVHTLLKKGVSIHARFTLNGLDDALIILKRIPKTYFEDEELQAACA
HVNLEQYEWLCSNNRGNKVEHVKSRVVTRAVKRRRKCRHWIYFDKDTLNLNYKYFDKKVT
ASMASKICNAKHDCLVFHRKMELEDLTESAYFKVEPSPINFAKLKSCPDVKYVQKKTDGT
FSVIRFFRNMTKGDLIQRMDLFCRFIPDSHTITLLSRADFYACKRGESMHMCTNKHRILH
YKFSNAPHAAIEQITNIISDTRGRKGIHIEYAIENVQEMYEEDGRRYEAKYTGTLTEYKR
NEDKTFKSLLAPHLTPVNKPYNINHLYEQYGNFDEELEDKLRSGFISYDTYVTAKDNWGR
CATGKGACI
(SEQ ID NO: 63)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
YO61_CAEEL (P34600) HYPOTHETICAL 84.7 KD PROTEIN ZK1098.1 I	36	0.95
Q9ZAJ8 (Q9ZAJ8) BONT PROTEIN	36	1.2
Q01794 (Q01794) MAJOR SURFACE ANTIGEN MSG1 (FRAGMENT)	36	1.2
Q9X708 (Q9X708) BOTULINUM NEUROTOXIN TYPE B (FRAGMENT)	35	1.6
GLND_HAEIN (P43919) [PROTEIN-PII] URIDYLYLTRANSFERASE (EC 2	35	2.1
BXB_CLOBO (P10844) BOTULINUM NEUROTOXIN TYPE B PRECURSOR (E	35	2.1

CT1060
Nucleotide
Genomic coordinates:
Start: 230616
Stop: 231582(SEQ ID NO: 64)

Amino Acid
MCTLKTYKMTTSTEISKNLSDVLSIKATGDWCSNIKTVFSPFTEGKGNLPNSLPFTRSPN
TTCGSREAANATEHFITVFAKDKYERKRVKRTIGFTLDNTKELTPNRYLVADVYSWQEEK
MVFEGFCVPPGKSGTFVRYSNEDKSFLLADTGRYMKKKYDDPENKTSSGGDDDDDDDDDD
DDNNNVDVYEENDPRNVFEVEKDEKYACTFSILVYRAMKKSPPVCRGLLVETDGPSSHPK
RAPSAFNPFGGSSMLNGYGAGADALEEEDEVDGVPERERITNFALKRGPATGQNFVSVKL
EHDGSKADLYNVTCFSKQRGV
(SEQ ID NO: 65)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
O97300 (O97300) PFC1035W PROTEIN	51	1e-05
KEX1_YEAST (P09620) CARBOXYPEPTIDASE KEX1 PRECURSOR (EC 3.4	47	2e-04
Q83970 (Q83970) (CPV)	46	3e-04
SIS2_YEAST (P36024) SIS2 PROTEIN (HALOTOLERANCE PROTEIN HAL	46	3e-04
YB00_YEAST (P38114) PUTATIVE 126.9 KD TRANSCRIPTIONAL REGUL	45	6e-04
O77384 (O77384) PFC0760C PROTEIN	45	8e-04

Comments:

TaqMan Primer/Probe Sets:
5'start=477
5'stop=500
3'start=555
3'stop=578
5'primer=CGATGATCCAGAAAATAAGACCAG (residues 477 to 500 of SEQ ID NO: 64)
Tm5=57.85
3'primer=TCGTTTTCTTCATACACGTCAACA (residues 555 to 578 of SEQ ID NO: 64)
Tm3=58.34
probe1=ATGACGATGACGACGATG (residues 515 to 532 of SEQ ID NO: 64)
probe1start=515
probe1Stop=532
direction1=Forward
Tm1=69.04
score1=1.95
length=102

CT1061
Nucleotide
Genomic coordinates:
Start: 231602
Stop: 232799(SEQ ID NO: 66)

Amino Acid
MQLILSHHLTMAGRVELVTGPMFAGKSTYLKNIYQQENGGNKHCLFVKHSLETRYGCGTG
TIVTHAGEVIEGCTTVSSIKELISVLPEVVDVILIDEGQFFTDLVLVNRLADKGKRIVIA
ALDGTSDQQMFSPIHKLLPYTNSIVKLASKCMICKIDTKEAPFTVRFGNDNDNNVICVGG
AEMYAAACRDCYKKINKKKNKGKLVVLEGGDRCGKSTQAKLLLTNKNSPLYGGEYMCFPD
RSSHTGKLINDYLTKKIELDDHAAHLLFSANRWEVCSKIKQLLDDGIHVVMDRYYYSGIV
FSLARGVDTVEWCSASDEGLPQPDLVLLMLLDVEKCSNRDTFGVERFETNSIQERARALF
LDLANKDEKNVWIKVDARGTIEEVQTKIINIVYNIVEE
(SEQ ID NO: 68)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
O74528 (O74528) THYMIDYLATE KINASE	165	6e-40
KTHY_HUMAN (P23919) THYMIDYLATE KINASE (EC 2.7.4.9) (DTMP K	159	3e-38
KTHY_MOUSE (P97930) THYMIDYLATE KINASE (EC 2.7.4.9) (DTMP K	157	1e-37
KTHY_CAEEL (Q22018) PROBABLE THYMIDYLATE KINASE (EC 2.7.4.9	148	8e-35
KTHY_YEAST (P00572) THYMIDYLATE KINASE (EC 2.7.4.9) (DTMP K	143	2e-33
KTHY_SCHPO (P36590) THYMIDYLATE KINASE (EC 2.7.4.9) (DTMP K	141	6e-33

CT1062
Nucleotide
Genomic coordinates:
Start: 232848
Stop: 233334(SEQ ID NO: 68)

Amino Acid
MLPRKTLPDTENGYFVLDESLLEKVYYDNNNELIVRVGGIYMQICKSKYIFHHDDPERFF
YSVLEDYHPIKEIVERLAEEDGVFLGPWEFLSRKQVNLQHGCYKALLSLPEDKYCNLLLP
QQMKTNLEKMEEIQRTRLIHSRTYNTPQIELSDQLDGCVIC
(SEQ ID NO: 69)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
O60678 (O60678) PROTEIN ARGININE N-METHYLTRANSFERASE 3 (FRA	31	5.4
P95966 (P95966) ORF C04027	30	9.3
Q9ZW94 (Q9ZW94) F5A8.4 PROTEIN	30	9.3
O58387 (O58387) 358AA LONG HYPOTHETICAL PROTEIN	30	9.3

TaqMan Primer/Probe Sets:
5'start=223
5'stop=245
3'start=309
3'stop=330
5'primer=GAACGACTAGCAGAAGAGGATGG (residues 223 to 245 of SEQ ID NO: 68)
Tm5=58.17
3'primer=TGGCAATGACAAAAGAGCTTTG (residues 309 to 330 of SEQ ID NO: 68)
Tm3=58.99
probe1=AAGTGAACCTCCAACACG (residues 284 to 301 of SEQ ID NO: 68)
probe1start=284
probe1Stop=301
direction1=Forward
Tm1=68.99
score1=1.96
length=108

CT1063
Nucleotide
Genomic coordinates:
Start: 236678
Stop: 238604(SEQ ID NO:70)

Amino Acid
MVASTPCPGPGPVPTQELLSTNFLEAHKLVVELLLPSYSSDVVYCDSETYTKPIPIFGNK
SIVSTIGDYVLSNPNEDVSYQMVSSVLEKFPLLFHCTYKTNEEDKGIPLWKKLYNKRKFK
LLNSLLVHNNKNWTPVPAIPFDRENICDASGRSVLMSEIMSTSTFQTICKNNTHYLFDML
NMERGKQGGSFLHFFASRKNSFTNFENEEMDSHVLSNIAKFICNEKEKLDSFIPANGKIP
CPDKTNDEGYIPLEIAIMEDNYPALLYLVCRYGASWANTYGDHNESLKAFAIRNDAKDCL
EIIEFISDHYSFNKNVTKEEFVKEKTVECVGCLYDIEDEKRCYKLPCGHFMHTFCLSNKC
SKANFRCVKCFQTFDDTIFRKCPPTIQWKMGINQTTNHKEMDLFNRAFDTYLDFICSYNV
KLDKKSKPKHKPENKKVEEELAKRTAEIEEAIKKKEEELAKRTAEIEEAIKKKEEELAKR
TAEIEEAMKKKEEEELSKYNKIIEKGKRRLNEECVKLRDISTAAINMYKEKVRINGVLLK
DSDQELAEAKERLRKILLLEEETKLDRFLFRPKRVEERIFLTKDDETLAFKLALEKKTED
IIAKKNNQKGSERRDGEYTITSHIEKLPQSTALASVCVLNE
(SEQ ID NO: 72)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
Q26938 (Q26938) KINETOPLAST-ASSOCIATED PROTEIN (KAP)	74	3e-12
Q9ZIU2 (Q9ZIU2) VIRULENT STRAIN ASSOCIATED LIPOPROTEIN	73	5e-12
O50870 (O50870) HYPOTHETICAL 54.3 KD PROTEIN	73	5e-12
Q9ZU69 (Q9ZU69) PUTATIVE VICILIN STORAGE PROTEIN (GLOBULIN-	68	2e-10
O23230 (O23230) TRICHOHYALIN LIKE PROTEIN	62	1e-08
MNN4_YEAST (P36044) MNN4 PROTEIN	62	1e-08

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 362 to 1 of CT1063: this corresponds to nucleotides 238163 to 238524 of the genomic reference sequence.

TaqMan Primer/Probe Sets:
5'start=775
5'stop=797
3'start=850
3'stop=872
5'primer=GAAGACAATTACCCTGCATTGCT (residues 775 to 797 of SEQ ID NO: 70)
Tm5=58.33
3'primer=GCAAACGCTTTGAGAGATTCATT (residues 850 to 872 of SEQ ID NO: 70)
Tm3=58.56
probe1=TAGGTATGGAGCATCTTG (residues 810 to 827 of SEQ ID NO: 70)
probe1start=810
probe1Stop=827
direction1=Forward
Tm1=68.95
score1=1.95
length=98

CT1064
Nucleotide
Genomic coordinates:
Start: 238658
Stop: 239438(SEQ ID NO: 72)

Amino Acid
MSTCSNLLSVFGGGDWTTTFPFDLVHTRQECDKKREQDYSFFITETCKGENIGIHSYEHT
SKIIDTGNNDSTSIEELEVLNIYKAINHLENILKLNKGEKIILMDVETMILETHKILMKG
ILPKGKNGSFSTCVRFAVNKNNERHYYPVFETEKEAFNSIQNLVDYYNEIVAHTNDQIKI
IKACAYFMYNFLTLHPFNDGNGRTARLLYSFLLKGNGIVPHFSPITHPRDQFVDTLVYFR
EHGDGRPLLYVLLESIKNK
(SEQ ID NO: 73)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
Q23544 (Q23544) ZK593.8 PROTEIN	50	2e-05
Q9ZHQ9 (Q9ZHQ9) HYPOTHETICAL 26.1 KD PROTEIN (FRAGMENT)	44	0.001
O68899 (O68899) HYPOTHETICAL 29.5 KD PROTEIN	43	0.002
Q48249 (Q48249) PLASMID PHPM180, COMPLETE SEQUENCE	43	0.002
O75406 (O75406) HUNTINGTIN INTERACTING PROTEIN HYPE (FRAGME	42	0.004
AAC96089 (AAC96089) HYPOTHETICAL 23.9 KD PROTEIN (FRAGMENT)	42	0.004

Comments:
EST confirmation of the predicted transcript:
Nucleotides 1 to 677 of CT1064: this corresponds to nucleotides 238717 to 239393 of the genomic reference sequence.

TaqMan Primer/Probe Sets:
5'start=397
5'stop=419
3'start=450
3'stop=472
5'primer=TGCGTACGCTTTGCTGTAAATAA (residues 397 to 419 of SEQ ID NO: 72)
Tm5=58.67
3'primer=TGAACGCTTCTTTCTCTGTTTCA (residues 450 to 472 of SEQ ID NO: 72)
Tm3=57.92
probe1=AATGAACGGCATTACTAC (residues 424 to 441 of SEQ ID NO: 72)
probe1start=424
probe1Stop=441
direction1=Forward
Tm1=68.96
score1=1.88
length=76

CT1065
Nucleotide
Genomic coordinates:
Start: 240712
Stop: 241192(SEQ ID NO: 74)

Amino Acid
MEDLKSTIERVYEERVENLEQWTNTVEEEERTVSAIDSVLEEQKRALDAWEAAIKERENDLAVKEGISALVFNAADAKTRKELINTWIAERETSEKRRKEATSTNNQLKNQMSSLVNTTKTLKEKYNKYYRRSAILNMQYINNKRDYEASQFWVYTNNA
(SEQ ID NO: 75)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
RADI_HUMAN (P35241) RADIXIN	43	0.001
RADI_PIG (P26044) RADIXIN (MOESIN B)	43	0.001
O40947 (O40947) ORF 73	42	0.002
SSP5_STRGN (P16952) AGGLUTININ RECEPTOR PRECURSOR	41	0.005
Q9Y489 (Q9Y489) CENTRIOLE ASSOCIATED PROTEIN CEP110	41	0.005
Q21952 (Q21952) SIMILAR TO MYOSIN HEAVY CHAIN	41	0.005

Comments:

TaqMan Primer/Probe Sets:
5'start=228
5'stop=249
3'start=297
3'stop=320
5'primer=CGCCAAAACACGTAAAGAATTG (residues 228 to 249 of SEQ ID NO:74)
Tm5=58.34
3'primer=TGATTATTGGTAGAGGTTGCTTCC (residues 297 to 320 of SEQ ID NO:74)
Tm3=57.45
probe1=AATACGTGGATAGCCGAA (residues 253 to 270 of SEQ ID NO:74)
probe1start=253
probe1Stop=270
direction1=Reverse
Tm1=68.84
score1=1.84
length=93

CT1066
Nucleotide
Genomic coordinates:
Start: 241184
Stop: 241505(SEQ ID NO: 76)

Amino Acid
MHKFSNKFYFIIKGVLIIIFVPDVVFSIFLLPPLGVRHKNGGGGNEEQKSGPSQKHHIPG
PVLIFVLIIVIVGSVVIIIGVLISVRIAVLLWSHPYIHDGQDEDTN
(SEQ ID NO: 77)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
Q19507 (Q19507) F17A2.11 PROTEIN	33	0.78
Q37367 (Q37367) NADH DEHYDROGENASE SUBUNIT 1 (FRAGMENT)	29	8.9
PSC_DROME (P35820) POSTERIOR SEX COMBS PROTEIN	29	8.9
YG35_YEAST (P53273) HYPOTHETICAL 117.0 KD PROTEIN IN ASN2-P	29	8.9
AAF05147 (AAF05147) ORF33	29	8.9

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 452 to 1 of CT1066: this corresponds to nucleotides 241246 to 241697 of the genomic reference sequence.

CT1067
Nucleotide
Genomic coordinates:
Start: 241774
Stop: 243409(SEQ ID NO: 78)

Amino Acid
MFRQFCSLYLLQRRVNDNLRSTASASAAASLKGDGTEFITGEPPSHKMRGPSYSVLGPDP
CEDPERVYVDIVVSILQTNNIQVTKEWELFSDKLRKLGPWIDRSGIENNGEGEEDGDENE
DGGGNGGRIEDREAHRRKMMKKLSFVGREDPVAVDLPTWRENSTEFARRLTLKELCDLIV
ECGCIKSKEELFDFIFEEPWEIKEAADVRGMANRSKFTKESLIDWFFEFDTYSKCVVFFE
AVNWYLKSQASPISLVLDDIYCCVFSYIRRQTFLTRAKNPSLTVASSFSPTPDTKLLAID
ECVQHFLKSDINISQMALTERDCFFPLLTEMPRQQKKVNTFLDTMKRPTLSLLPSTSSSS
SSNNKRKRNTAAANILLPVYRSNFSTASNNKRLKTDDGENASACILIEGYANGKISPIRI
MVRKSTIIPEVFNHLLFPVFASKDTGANILFFIKMKSFASASLLLPGLFRHPKQFLNGPC
KWMTLAENNINDNNINSSTMWSYTLADYCPLGYYTQESPQPYQTCGNFTSTTNKRLQNVQ
PLYF
(SEQ ID NO: 79)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
CAB38842 (CAB38842) HYPOTHETICAL 35.2 KD PROTEIN	39	0.061
CAB52581 (CAB52581) CONSERVED HYPOTHETICAL TBC DOMAIN PROTE	39	0.10
O84402 (O84402) RIBONUCLEASE FAMILY	37	0.31
Q59085 (Q59085) RNA POLYMERASE SIGMA-54 FACTOR	37	0.31
O80815 (O80815) T8F5.22 PROTEIN	35	1.2
PI4K_DICDI (P54677) PHOSPHATIDYLINOSITOL 4-KINASE (EC 2.7.1	35	1.6

Comments:

TaqMan Primer/Probe Sets:
5'start=717
5'stop=740
3'start=791
3'stop=814
5'primer=TGAAGCAGTCAACTGGTACTTGAA (residues 717 to 740 of SEQ ID NO: 78)
Tm5=57.74
3'primer=TTTGGCGTCTTATGTAGGAAAAGA (residues 791 to 814 of SEQ ID NO: 78)
Tm3=58.08
probe1=ATCTCAAGCGTCTCCAAT (residues 741 to 758 of SEQ ID NO: 78)
probe1start=741
probe1Stop=758
direction1=Forward
Tm1=68.99
score1=1.99
length=98

CT1068
Nucleotide
Genomic coordinates:
Start: 243216
Stop: 243798(SEQ ID NO: 80)

Amino Acid
MDDSSRKQHQRQQHKLFHDVELHASRLLSSGLLHPREPSTLSDMRQFYFDYKQETTKRAA
IILLNTLLEYYRTPSEEWEIPFNLLLNVMNNKWSTLIPGVKISAGIISKLPWTMKTMYEI
VSSPNNNNNNGDYYSTCRRMVMEYPIGGLLHTPAITNKYPRSRMVTCTKGKDHQKLYDIS
RQMFDIIEANGQL
(SEQ ID NO: 81)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
P3K3_DICDI (P54675) PHOSPHATIDYLINOSITOL 3-KINASE 3 (EC 2.7	32	3.0
O01590 (O01590) K09H11.1 PROTEIN	31	6.7
RRPL_DUGBV (Q66431) RNA-DIRECTED RNA POLYMERASE (EC 2.7.7.4	31	8.8

Comments:

TaqMan Primer/Probe Sets:
5'start=234
5'stop=257
3'start=308
3'stop=331
5'primer=GGAAATTCCGTTTAATCTCTTGCT (residues 234 to 257 of SEQ ID NO: 80)
Tm5=57.99
3'primer=GGAGTTTCGATATGATACCTGCAC (residues 308 to 331 of SEQ ID NO:80)
Tm3=57.75
probe1=GAGTACACTCATTCCAGG (residues 279 to 296 of SEQ ID NO:80)
probe1start=279
probe1Stop=296
direction1=Reverse
Tm1=68.82
score1=1.82
length=98

CT1069
Nucleotide
Genomic coordinates:
Start: 244241
Stop: 244856(SEQ ID NO: 82)

Amino Acid
MDLSFTLSVVSAILAITAVIAVFIVIFRYHNTVTKTIETHTDNIETNMDENLRIPVTAEV
GSGYFKMTDVSFDSDTLGKIKIRNGKSDAQMKEEDADLVITPVEGRALEVTVGQNLTFEG
TFKVWNNTSRKINITGMQMVPKINPSKAFVGSSNTSSFTPVSIDEDEVGTFVCGTTFGAP
IAATAGGNLFDMYVHVTYSGTETE
(SEQ ID NO: 83)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
O85179 (O85179) FLAGELLIN A	34	0.60
FLAA_CAMJE (P22251) FLAGELLIN A	34	0.60
BAA83944 (BAA83944) UNKNOWN	34	1.0
FLAB_CAMJE (P22252) FLAGELLIN B	33	1.8
AAC25644 (AAC25644) FLAGELLIN A	33	1.8
AAC25648 (AAC25648) FLAGELLIN A	33	1.8

Comments:
EST confirmation of the predicted transcript and hits to pblic SBV sequences:
Nucleotides 1 to 803 of CT1069: this corresponds to nucleotides 244132 to 244934 of the genomic reference sequence.
Hit to public sequence gi|6856162|gb|AF173993.1: CT nucleotides 1 to 615 match nucleotides 323 to 937 of the public sequence with a 100% homology, a score of 1219 and an Evalue of 0.

CT500
Nucleotide
Genomic coordinates:
Start: 2425
Stop: 1537(SEQ ID NO: 84)

Amino Acid
MKNSRQRSGVWRGNSCLYKSFYFSGAIIECKKIRIIMMFLLLSLILFVCFVGVVVGVIFM
SRPNKTTTTSNKKTKKDKEKEKEDDTEGAVLGRREPENRPIGRDEEGAVEDGKEEEEVFE
FEQPSVNTGSNTGGGGTGTVPGEGLLPPPPPTPTPTPPPTPTPTPPPPPTRTPSPSSSLG
EDDDDDIDIDFDDNDIDEFLDSGEEMEEDEEEEDLDTLLSRLETGMSGEEVDFDASSAYI
QPDPVVVKNIERSDYTLDPMESWKVLNRSEGDIRFFVDRGITNKIKAMTEDLKEL
(SEQ ID NO: 85)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
Q48373 (Q48373) CHITINASE PRECURSOR	64	2e-09
O86476 (O86476) CLUMPING FACTOR B PRECURSOR	59	4e-08
O92451 (O92451) ACMNPV ORF91	58	9e-08
Y091_NPVOP (O10341) HYPOTHETICAL 29.3 KD PROTEIN (ORF92)	58	9e-08
Q69023 (Q69023) (B95-8 ISOLATE) U2-IR2 DOMAIN ENCODING NUCL	57	2e-07
Q42421 (Q42421) CHITINASE PRECURSOR	57	2e-07

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 244 to 513 of CT500: this corresponds to nucleotides 1979 to 2248 of the genomic reference sequence.

TaqMan Primer/Probe Sets:
5'start=419
5'stop=440
3'start=505
3'stop=523
5'primer=TGCCTGGAGAAGGTTTGTTACC (residues 419 to 440 of SEQ ID NO: 84)
Tm5=59.11
3'primer=GAGATGGGGTTCGTGTCGG (residues 505 to 523 of SEQ ID NO: 84)
Tm3=59.88
probe1=CCTCCTACTCCTACTCCT (residues 448 to 465 of SEQ ID NO: 84)
probe1start=448
probe1Stop=465
direction1=Forward
Tm1=69.04
score1=1.95
length=105

CT501
Nucleotide
Genomic coordinates:
Start: 7645
Stop: 7042(SEQ ID NO: 86)

Amino Acid
MTMWNKIVITTKRMNWPMVVGVFFILAITALAVALYIRHASKQEKYSTSHINEQFTAKQL
PVTYLSKTGKLKDMHLTHSDFMAYVDVHNRTKTLKHPMCTDEAGWAHFCLLASAEAYRRI
RYGRGEFGPEKHSLAETIQSTVQDMSEPYITHIFKKNTDVDGHGMQSVLEKNRNKIRMGD
GKTSSETYNLSDKSISIVGV
(SEQ ID NO: 87)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
Q21859 (Q21859) R09D1.3 PROTEIN	34	1.0
Q9Y3S0 (Q9Y3S0) EMDC II PROTEIN	32	4.0
AAD25099 (AAD25099) METALLOPROTEASE DISINTEGRIN CYSTEINE-RI	32	4.0
O31548 (O31548) YFJL PROTEIN (RIBOSOMAL PROTEIN L6-LIKE PRO	31	5.3
Q44602 (Q44602) PHOSPHORIBOSYL ANTHRANILATE TRANSFERASE	31	6.9
CAB52230 (CAB52230) HYPOTHETICAL 33.8 KD PROTEIN	31	6.9

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 587 to 1 of CT501: this corresponds to nucleotides 6996 to 7582 of the genomic reference sequence.

TaqMan Primer/Probe Sets:
5'start=245
5'stop=266
3'start=315
3'stop=332
5'primer=TGGCATATGTTGATGTGCACAA (residues 245 to 266 of SEQ ID NO: 86)
Tm5=59.44
3'primer=AGCAGGCAAAAGTGGGCC (residues 315 to 332 of SEQ ID NO: 86)
Tm3=59.78
probe1=ATGTGTACTGACGAGGCT (residues 292 to 309 of SEQ ID NO: 86)
probe1start=292
probe1Stop=309
direction1=Reverse
Tm1=68.96
score1=1.96
length=88

CT502
Nucleotide
Genomic coordinates:
Start: 8502
Stop: 7641(SEQ ID NO: 88)

Amino Acid
MSSGSINNHPSSNMDTNKMEEGEEQDFDVLELDYSKIIHDITAMLSVAAPPPNSILDASD
GLIATASATAPAAETGNSNRMRLDKDVCQLIERDIELVKSDTIEVDSIIRQLLYFGESAS
EKNIKTNSTEKEPVYFPKEPKGEAVKLAKNTPVLDTITKLDWMANICQSNKIGVENLASA
LQSGQLIWTTFPAAVYASLDSFYHIAIMWKLLGSFINIEALSKGSKDNLLPRDDIQVVHA
KQEIAAMLQSRQNILGRGPSEYPPVPITAILSRTIIPLLRNFSEKL
(SEQ ID NO: 89)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
O43631 (O43631) SPINDLE POLE BODY PROTEIN SPC98 HOMOLOG	38	0.063
O60853 (O60853) PROTEIN ENCODED BY SACCHAROMYCES CEREVISIAE	38	0.063
O60852 (O60852) PROTEIN ENCODED BY SACCHAROMYCES CEREVISIAE	38	0.063
AMPR_HUMAN (P15514) AMPHIREGULIN PRECURSOR (AR) (COLORECTUM	34	1.2
BYN_DROME (P55965) T-RELATED PROTEIN (TRP) (BRACHYENTERON P	33	2.1
AAB32396 (AAB32396) T-RELATED PROTEIN	33	2.1

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 1 to 753 of CT502: this corresponds to nucleotides 7704 to 8456 of the genomic reference sequence.

TaqMan Primer/Probe Sets:
5'start=315
5'stop=336
3'start=392
3'stop=412
5'primer=TGACTCCATTATTCGCCAACTG (residues 315 to 336 of SEQ ID NO: 88)
Tm5=58.70
3'primer=TGGGGAAGTAAACTGGCTCCT (residues 392 to 412 of SEQ ID NO: 88)
Tm3=58.70
probe1=TGGAGAATCTGCATCAGA (residues 345 to 362 of SEQ ID NO: 88)
probe1start=345
probe1Stop=362
direction1=Forward
Tm1=68.85
score1=1.85
length=98

CT503
Nucleotide
Genomic coordinates:
Start: 9248
Stop: 8552(SEQ ID NO: 90)

Amino Acid
MDPGASAASRRALWSSTVTNTRHYQQQLNRALNKIEEEDDVEEEHGQVTTTNKEMASTST
SSSSSSSSSPTSSAIPSSDEEEEEEEEYDSESDTNVDSLLGEEEEEDSDTESTSADANFL
RSSSRNSTTRNRLIKKYVDRFIKYEKDILLADRNKRKKRHRNRQPQIHKLNNKRLKKPTD
KKQKTNKKKTWRRLPKFIKKMSPASRLKFFSACIISGIKITSIIVLSIMAL
(SEQ ID NO: 91)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
NSR1_YEAST (P27476) NUCLEAR LOCALIZATION SEQUENCE BINDING P	56	2e-07
FKB4_YEAST (Q06205) FK506-BINDING PROTEIN 4 (PEPTIDYL-PROLY	55	4e-07
GAR2_SCHPO (P41891) GAR2 PROTEIN	52	5e-06
O95367 (O95367) CBF1 INTERACTING COREPRESSOR CIR	52	5e-06
SR40_YEAST (P32583) SUPPRESSOR PROTEIN SRP40	51	6e-06
O08904 (O08904) BRAIN X-LINKED PROTEIN (BRX PROTEIN) (FRAGM	50	1e-05

CT504
Nucleotide
Genomic coordinates:
Start: 13936
Stop: 9328(SEQ ID NO: 92)

Amino Acid
MAHKLLFLEEEDAKEIGTLSHPEPSFALYESETFRSVGFCKNVTDAYPKFLPRPMDINSV
QALAVRLALIQFYKGRGWKKNMSIIDLVKDKVERNFKVDKKTSGGFIIGDGTGVGKTREL
AAFVMSVILQEKALLDVQKHVGPSIFGQDSDKVITAINSGVWKRHPFFIWLTCSKPLFNS
CQQGMREVVTNSRGLRDPKFSWRKLQVPCANKPTSFKSDGKSGSMTVDVENSVSSAKDSV
DIRFFTLRDVKEFHSKRSSRSIGDFLTETPTILFMTYSDLRTNLEFVLKFITGGTDLDSN
KVMPIDNFVTALLCDEFHKTQNISDSFRKELAKTWEEEDTRVLRNIQKRANPSVSDLINR
FKSAMSDDRNFKVKRMKSSNNKGRVTMSNYLKLLSQADAFRIFLEILKYDTFTVMASATP
FQSNADLHMIDHILRKSAPAYTSIQAFKEVSSATPDAMAEHSEYVTVFLEQVIKLLRNRG
QLVSRSISMAGVDCSTTNCKASPLQKYAIDELASYCLNARQVLIDSEKVGGHVRRAFTKI
IREHQEGGILEEEDVEKLVAEINSPSRKRKRAANDDDLYEVMENIDRRFKVVVVRDRDVA
HDGKTTLRSIVQDAIKTYSQKKDALSNGGGGIITSPEVDISSIDMVAQDLYDAIKKKEKP
SKGKTDFNEDYDDGANEEDGWGEVFDDECFEKLRRQYFINTASTSVAACKGALLNIKATS
VTDAVKRLRTTNESKKMVMSLEQTGDSFLKNLTTRILQTIAKDESDAKYGIVDVGTFDSS
PVANTIFSGYRLLCRAVMMASAFTISLKNKTNRRTSPAHVMLVPSVPDTEPLMALAGNPI
DSITQSIGEDSNAEITNRKLCSRITNRGLFLVKNNTKTANTNKCISAFNNTKEVDVIMLG
PKGNTGLSLHDSSNNSMYAKRYHCVLDVPYNAIAFLQTIGRTHRNGQLSVPQFLIFSTDS
PAERRFFDSLDKRIKDSKAGTYADRYSNNSIDIAAAVMREQFIDQGLVLKTMGNIVQIVT
ASMTKVHLMEHFSKMMMRTNRGGVAFVEGLTLENGIFTEVIVLAMHIALVVIGAQNKITS
SDDLGHALSFTSVLPHNQILSIVKSASQFVFSNLCLHLVHFKSDCDNLLPREKRVRDAAS
ALIDTLNTKNNEVTSKTNKIESDAPSLTALMLPSGPRNRKMDVFSNIMAYNNNNGMDFDE
DVPDNDEDEGCLPLQEENATTLALSNFPHDYDRAIKDAHQLVTVRIVGQGEKEGVIPISE
CLDVPELDMTNLIPVVTATNVIQSLAKENPGLLFTIHNAALAHSHREGYGGSHLLGLAKK
LSRGFINFRQFQNQLFSPKKESKIMYDIFLSVKAIMARDDRYDGLCDMRMNSMMDASFLK
VRKKPECVFITKLLDKNFRRHIINDEEEETRERFGGEEEEEDDDEEFEDEEEEQAEREWG
EEEGESAYDISVINDKNNTIGHDVDIILCNRKKLTLTKENSVFVNEHIDSFMVGNLIGAE
GSLIQICFDNCTGEFEGLPKFCLYDSSSKDKDTIP
(SEQ ID NO: 93)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
O01940 (O01940) STRAWBERRY NOTCH (SNO)	72	3e-11
Q9Y2G9 (Q9Y2G9) KIAA0963 PROTEIN	62	3e-08
O75257 (O75257) R31180_1	62	3e-08
O01737 (O01737) F20H11.2 PROTEIN	62	4e-08
O85862 (O85862) PROBABLY METHYLASE/HELICASE	59	2e-07
O64516 (O64516) YUP8H12R.3 PROTEIN	53	1e-05

TaqMan Primer/Probe Sets:
5'start=2131
5'stop=2154
3'start=2210
3'stop=2233
5'primer=GGTGCACTATTGAATATCAAGGCA (residues 2123 to 2154 of SEQ ID NO: 92)
Tm5=59.03
3'primer=CAGTTTGCTCTAGTGACATGACCA (residues 2210 to 2233 of SEQ ID NO: 92)
Tm3=58.06
probe1=TTCTGTCACCGATGCAGT (residues 2157 to 2174 of SEQ ID NO: 92)
probe1start=2157
probe1Stop=2174
direction1=Forward
Tm1=69.00
score1=1.99
length=103

CT505
Nucleotide
Genomic coordinates:
Start: 16983
Stop: 14064(SEQ ID NO: 94)

Amino Acid
MDERRRDPLLYPTNRSMRFTAQITLFVTVFVLGCIFALVCAAMAYNVAKPMSVNFQAIHE
LGMKSKLKAVQGANPEKTLEEYLEARGRHDGVEDASNYPPHPALLDMMNLTVKGNKWNVP
SETKERNSRFESHDLAANRSSSLLVPEHHIDRLSEATIEKSNKYLDAVSGKKFRQRMVNL
KDNIEKDDTELYDSLFGVHDIHHHSASGVSGDAPPPPPSTSEGHDEDVDILAYNTGGYCS
NPVPLKEGQTCTSVCYTSRAVRVMTPFVAGGTFITHKSGEDPKPYCWSGNVPGDHIETSP
TTGERVVKECSVHTSIVVLTDDGGWQCRPKYPTYFGGSGGTSMTACAFNPSTHKGPPPPS
SSTPIYYDVLKKQQIRNHTEFRNSSYISKLRQSSSLAEFKIKCNDPEFLYKNPITCFCNN
KKDVLNNDLLSQDVTKDMKFRGMYECMENPCVMMPNIDPSFVTFDVSTMKCVPGVNNPQD
SNRHAIIGDDRTPLVGTVPAMGIFLADQSKRGDQIHQQRPKSSIDETTAKKIALAQAPII
TPLNLDATNTSKNVLFVPIPSTVLPPLENIPHVIIRPSSLLHRSCLAPVLNKPSSGQHRP
FCTAPFYIEPAANVLAGNIPQKPYEHSMLATECLRNSRMVSGSVHGGSELLFSTLLSQNK
PSSYIRTPPGGTPAPEYNSTGDQRLEEIRDFFERNFNDERRLSQTEYVIKKHARGMRTSE
IYLKSSSWDSLMKRKEFLRHIIKKSEDTFVLKEGLLMRSYGPYAATVLARDMFDLDYLKG
KPASKTSSTLKVSNPLQYAFPTSYSVLPEEGATDDIFSVDHNRIFDSETIPSYFDCSNVT
PGSEKLFGTSSSSSEYRVDIDDDAWGLQSFRLDHNPKSGPVVQSDPRLAFDASNISSTPE
GATITPLSLFKKSLVEWGHKKADVQETSWFRDGVDTSEAYRRLLVETSMAVRNSWFSLAW
ENKNYYFAKNSS
(SEQ ID NO: 95)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
CUP5_GALME (Q24998) PUPAL CUTICLE PROTEIN PCP52 PRECURSOR (	46	9e-04
CFHD_HUMAN (Q02985) COMPLEMENT FACTOR H-LIKE PROTEIN DOWN16	38	0.33
P89911 (P89911) PROTEIN KINASE	37	0.57
CAB39619 (CAB39619) AIG1-LIKE PROTEIN	37	0.57
CAB53064 (CAB53064) DJ15D12.2 (FHR-3 (FACTOR H-RELATED PROT	37	0.75
Q24552 (Q24552) TF125 PROTEIN	36	0.98

TaqMan Primer/Probe Sets:
5'start=1446
5'stop=1466
3'start=1511
3'stop=1532
5'primer=CAGGCATGCAATAATAGGCGA (residues 1446 to 1466 of SEQ ID NO: 94)
Tm5=59.66
3'primer=CTTTTAGATTGGTCGGCCAAGA (residues 1511 to 1532 of SEQ ID NO: 94)
Tm3=59.21
probe1=GACAGGACACCGTTAGTG (residues 1468 to 1485 of SEQ ID NO: 94)
probe1start=1468
probe1Stop=1485
direction1=Reverse
Tm1=69.00
score1=1.99
length=87

CT506
Nucleotide
Genomic coordinates:
Start: 25878
Stop: 25197(SEQ ID NO: 96)

Amino Acid
MASVFEDPADLFANMDLTGKVPTRPNILFFEGLLPNSGKEIMENRLIHKGKCGAFEADTQ
LAYFFPSNNEENTKKLNIGFQIKSNCLSFFIRDFLNDWLEEIKDCGPYCTFSQYMDGDKE
IFGNSVFGQDFTIVAMDWIDKGVTFYIFVDGSDSMENMASLWMCDKLKRMNANVVKVFVD
NASKPKFSVCKTCRWEFPGPVSYVIEGHGMGHSDLSCDEISEFLVQ
(SEQ ID NO: 97)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
AMY_BACCI (P08137) ALPHA-AMYLASE PRECURSOR (EC 3.2.1.1) (1,	35	0.44
Q85449 (Q85449) PROTEIN 8	32	3.8
Q85439 (Q85439) COAT PROTEIN	32	3.8
VP8_RDV (P17379) OUTER CAPSID PROTEIN P8 (STRUCTURAL PROTEI	32	3.8
Q85451 (Q85451) OUTER CAPSID PROTEIN	32	3.8
Q24284 (Q24284) PLC-GAMMA D	31	6.6

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 1 to 652 of CT506: this corresponds to nucleotides 25216 to 25867 of the genomic reference sequence.

TaqMan Primer/Probe Sets:
5'start=287
5'stop=307
3'start=351
3'stop=373
5'primer=ACGACTGGTTGGAGGAGATCA (residues 287 to 307 of SEQ ID NO: 96)
Tm5=58.18
3'primer=TGTTTCCGAAGATTTCTTTGTCC (residues 351 to 373 of SEQ ID NO: 96)
Tm3=58.28
probe1=AGGACTGTGGACCATACT (residues 308 to 325 of SEQ ID NO: 96)
probe1start=308
probe1Stop=325
direction1=Forward
Tm1=68.99
score1=1.99
length=87

CT507
Nucleotide
Genomic coordinates:
Start: 29077
Stop: 28330(SEQ ID NO: 98)

Amino Acid
MIAIANHKHDVSDALVGAHGAKINMLYGKSSTLSVTEAALLMFNDTALTQFAQRGYEPSI
PTILKAALDFSLQEEEPLVAATGLDVNKAPRSWPILNCRLGYIASSNYPWAEHIISGDKE
EIKRALEEHEKNANVRFDSDNCPVCLEDFSSTNIIRTTRCGHCIDEKCWDRLVLSTQRGE
ITRCPVCRERTSLRPDADQVKEMLVEPIVSCKRMAVPDEQVSCKRRRIGYNRYQFLINDV
WTDESETV
(SEQ ID NO: 99)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
Q9ZT52 (Q9ZT52) RING-H2 FINGER PROTEIN RHA1A	45	7e-04
CAB51420 (CAB51420) RING-H2 FINGER PROTEIN RHA1B	44	0.001
Q9ZT51 (Q9ZT51) RING-H2 FINGER PROTEIN RHA1B	44	0.001
CAB51421 (CAB51421) RING-H2 FINGER PROTEIN RHA1A-LIKE PROTE	44	0.001
O17099 (O17099) F42G2.5 PROTEIN	42	0.005
O16682 (O16682) ZK1240.2 PROTEIN	41	0.008

Comments:

TaqMan Primer/Probe Sets:
5'start=257
5'stop=279
3'start=308
3'stop=330
5'primer=TCAATAAAGCACCTCGTTCTTGG (residues 257 to 279 of SEQ ID NO:98)
Tm5=59.26
3'primer=CCAAGGATAATTTGAGGATGCAA (residues 308 to 330 of SEQ ID NO:98)
Tm3=58.96
probe1=CAATACTGAATTGTCGCT (residues 281 to 298 of SEQ ID NO:98)
probe1start=281
probe1Stop=298
direction1=Reverse
Tm1=68.81
score1=1.81
length=74

CT508
Nucleotide
Genomic coordinates:
Start: 30861
Stop: 29073(SEQ ID NO: 100)

Amino Acid
MAEAAPRYRQVLEEVLENIEPYMSFLDVFTERELALLNDIITSRNSPPVPSSSFKKLDNK
EEFRDIIYFFINNNTKSDSSPICEGMTFINALTTVCKTFRGLYENIHDDFLFVKYSLLVS
MDNGFLRRETHGIKFGTGDDSRTGFKFTSKEQAEEEREKVMRRIKKLDGVLASLKKSTSS
ARSGIVFYVEKCSSVIRFRLFSRIVNITSDYVAEMKKSAPLEPFDISFGYKYFVDESPCV
TKAKRLISNGNFIIGRPFSCLETSPSSVSTDFREEMNMDARSIARLNWTNEERASAYRSV
IIKSFLSSIEEEMVEEYCETTTKTVAEMAVEFVDVFIEKAETIQHFQTLYSIFDTMPKFS
AEMMDNILKNVAINEAVGSGLCGAILLWMINSRPFEEIDYNYFKICLREIMVRKKTDKLC
DNLIVKRIVSHKNVVITDPHEVKGYVRLCVKVSCFMEDLEAFLTKNPWLKHTYFDEKGNT
LLCYCIINKYSHTSKLVKQEKLNILKPSAKGMSPLMVCAAISSPFTTRVGIEILTTNSLA
FSFINENNENVFHAAAVATSCNFLDALAKKYKNIIYDFDRSIVNARRRAMVQRP
(SEQ ID NO: 101)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
CUL1_CAEEL (Q17389) CUL-1 PROTEIN (LIN-19 PROTEIN)	36	0.99
O23296 (O23296) HYPOTHETICAL 74.2 KD PROTEIN	35	1.7
Q57577 (Q57577) CARBON MONOXIDE DEHYDROGENASE CORRINOID/IRO	35	1.7
GIDA_COXBU (P94613) GLUCOSE INHIBITED DIVISION PROTEIN A	34	3.8
Q47427 (Q47427) PLASMID P15B GENES R, S, SC, SVM1, SVMR, SV	34	3.8
Q39068 (Q39068) CYCLIN 2A PROTEIN	33	5.0

Comments:

TaqMan Primer/Probe Sets:
5'start=742
5'stop=764
3'start=822
3'stop=845
5'primer=TCCAATGGCAATTTTATTATCGG (residues 742 to 764 of SEQ ID NO:100)
Tm5=58.75
3'primer=GATCTAGCGTCCATGTTCATTTCT (residues 822 to 845 of SEQ ID NO:100)
Tm3=57.51
probe1=CATCCGTGTCAACTGACT (residues 797 to 814 of SEQ ID NO:100)
probe1start=797
probe1Stop=814
direction1=Reverse
Tm1=68.91
score1=1.91
length=104

CT509
Nucleotide
Genomic coordinates:
Start: 37245
Stop: 36048(SEQ ID NO: 102)

Amino Acid
MAGTDIISSSSSGSSSSKKGGCIVSKKGKTIKGKNIVFKTSIKTSSSSEMMKKHKKRMEI
KDMVKKCASCKKVDYSSSTLENDALRASIESTCSALNRFPEIKYGEGEIGDVLSAIRLMA
GCLLAKNEKSFYKFFLRGFQFDKNGFMMLSEGMKRIEKMHTKIAKKVFGGCKAAPLKEDR
EGKIPCQEFHKPSSYKGEYTTPLPPTPAPVKVLPPLLPYKNVKNKPVFVPDLAVGEAKKP
CWVHKLFSDDPEERKRLFERHQAGRRDALMEDYGVIPNNDNEAEDTERFVSNALEYQAQM
LELLDTANMPPPASTPVRRGRTRIVRDYDASPVPSPYSSPLHTPFDAPNVNLNPGSGRMV
DRVRDGRRNTSRRTSAVMARRINQLQHQFLYYSSDSDF
(SEQ ID NO: 103)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
O01693 (O01693) COSMID T08B2	39	0.073
CAB52863 (CAB52863) PUTATIVE MEMBRANE PROTEIN	36	0.37
O01348 (O01348) ZINC-FINGER PROTEIN KLU (KLUMPFUSS PROTEIN)	36	0.48
Q9ZDN6 (Q9ZDN6) VIRB10 PROTEIN (VIRB10)	35	0.83
Q9Y2W9 (Q9Y2W9) ENDOCRINE REGULATOR	35	1.1
GAR2_SCHPO (P41891) GAR2 PROTEIN	35	1.1

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 1 to 973 of CT509: this corresponds to nucleotides 36148 to 37119 of the genomic reference sequence.

CT1070
Nucleotide
Genomic coordinates:
Start: 249425
Stop: 253221(SEQ ID NO: 104)

Amino Acid
MASSGGFFTGIDDLFKTVIQQEKQEKNKPTQAPETEPKPGPSQAPDPVPDPVPKTPTNFC
PPPPNPLPPPPPPPPKPSREERLKTSKIRLNKALSDIVEATNERVDALKENQALNTEYDK
KDNYFQVLKCSITPSVPTAIIGAHVKQVAKSSEIELAVNELDIKNKCSLVYNENESLKFF
RDHENLILQIAVQLFSRHDNTKCVGAEICVKGNEKNKFVNKLVVKKLPNAPSSSSTVLEI
RGATRNLLENNFNKGENNTVNENKDIPPSERANLDTTKAEISHVFSTLHRLDTKRKLFFK
GNTFYQRKPTFDNKFRWTEVIGWTESEASKQTTKSLDKPTDDNLFVLPHSFNNLADHLRL
KFKNVLYKNSTAHPGKRNYYKTQETLINPQIDSAKEYKMVFAEIDKCLDVLLAIGKNDKY
TKSTVIQYRGKFRRYLIFCYAFYALNKAKHSRAVSPLPFNFFNLFSFMYCHGPFLHSASF
LSTLTFVYQHMFFPMGTAAPSVSAKRLMDIDSALMKGGKGVGVRDFGSPSKTSLHTRTLV
SFLGFAEMAMGTMTALLSGVEVRVSPALQQRISKSLERWCDSVIFIYFTFVLFHRFSGAK
KVSLESALRLIMGQTHAHTNKVRAAKRCRIEAAEMEGVEEEEAGLTLSYAHLLGLPYSIQ
KALGLPVPKINPLMTASSSQYNLGDFVGVEQLLKAKREFPAEGETAGFLGMFDNLVKDSI
DKYYGEGAFSDVVENVKQGMEQNTPYDTSSALMTPIPKAFYEEEKDVPQQEENSTQQRYR
LNRDVEEYLMASPMKMVFVSILDKTNQKERFMSVGDIALLAVWCKRNVLKKDWNEYAIAK
GNYEWLGAKMCNHLLLADLVNFGILGDLKITNKLDTNTDTFHRDSDRLPSVADQKKFIKN
TSLSDRKQLALVHSCVNVSTRTHVGRVTATSWAVDALRTYTRGDKDMFAALSSSLDMYHL
GHTNSANFVPYFSRNYLCNEQENGLWGYTRRTSEKLAKEELGRGRLGGLNKVGVAKTELA
AAAIAISSALDMGEVEAVMDDSSKVRKIASTCLNVNAAKVSAAREKAREASIKRLLLATN
APAAGSSRNSNRFLLKDLWGFFSDPDKRQKLIKGEAVSVLCPNTGFLHAAVPDFVIEYSF
ESETSIVRLRLRLIKPEKQDEMVCPSTAPEANKKRKLVRNNQDAVLTLDDEDNIVKYNKY
DMVEDEEARERLRHQDKQSVIAARISKVCERKNPKKKRRLEDPELQSVDEQLIRELAAIA
Y
(SEQ ID NO: 105)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
SSGP_VOLCA (P21997) SULFATED SURFACE GLYCOPROTEIN 185 (SSG	64	8e-09
YPRO_OWEFU (P21260) HYPOTHETICAL PROLINE-RICH PROTEIN (FRAG	62	2e-08
O13305 (O13305) PROTEASE 1	61	5e-08
P93797 (P93797) PHEROPHORIN-S PRECURSOR	61	5e-08
AAD37432 (AAD37432) M-LIKE PROTEIN PRECURSOR	59	2e-07
Q54071 (Q54071) M PROTEIN PRECURSOR, MSZW60	59	2e-07

Comments:

TaqMan Primer/Probe Sets:
5'start=1884
5'stop=1904
3'start=1931
3'stop=1952
5'primer=CCGAATAGAAGCAGCGGAAAT (residues 1884 to 1904 of SEQ ID NO:104)
Tm5=59.32
3'primer=TGGGCATAAGAGAGTGTCAGGC (residues 1931 to 1952 of SEQ ID NO:104)
Tm3=60.21
probe1=GAAGGTGTGGAAGAAGAA (residues 1906 to 1923 of SEQ ID NO:104)
probe1start=1906
probe1Stop=1923
direction1=Reverse
Tm1=68.98
score1=1.98
length=69

CT1071
Nucleotide
Genomic coordinates:
Start: 253296
Stop: 255120(SEQ ID NO: 106)

Amino Acid
MRDDTFNQETAVKLVRWYTEYDCCCPLVNRVERLLGSFGGGVDATSVRSRPALYEEDKKG
DKCIPFRITSLIEGILLERALTKPDLAAAAFDVSEKLVYCSCNNTQGNFDVSSMTIWIDG
NNSKKYEVTCPSCTVEKISGGAESIHKKPMSLLAFFNNLVEKEAFAERIELKKLYLSLLT
GSAAGGGGMYKDSSQQSSFNGSWTSLLFHTSKKDKTRLEAEVLVSNKIKHTSRLQPRCVC
SDLLYALCSTTNNSASYAYKARNLCVIEGGEFLYFKYTIFEENGPFDSKTDLQSLVNNEP
VSETNSSALAASSSSLEDDDDCCDDDDDDDDDEDEKTKKKQPKKQTKKQKTTTSTLPPIS
KTNHDNMLMNVLKKGAVNGKRKMMDSLSGKKGQHSKKLKTSAAAGGGASSDVVAGENEEE
NNPSSVSPTNNRDRKDYVLPCPQIEEVTIFSQHRMNNNKLAESVVKHSVVINGNCLNLFV
TQHRKKYILPHENILFCPPLVQHVGFNKFRILTGVSCFFDRIEIVFSDQSDSVVLSNNAA
HSAILRLLSYIRENSLKRSVRTASVKGIDFVVKSQDTNIGIPLSNKEIRERQLCSASTLS
MLAGLGK
(SEQ ID NO: 107)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
Q20497 (Q20497) F47A4.2 PROTEIN	52	2e-05
KS1_HYDAT (P38978) KS1 PROTEIN PRECURSOR (HEAD-SPECIFIC PRO	50	6e-05
YIL2_YEAST (P40480) HYPOTHETICAL 123.6 KD PROTEIN IN POR2-C	48	2e-04
FKB4_SPOFR (Q26486) 46 KD FK506-BINDING NUCLEAR PROTEIN (PE	47	3e-04
Q06459 (Q06459) NUCLEOLIN	46	9e-04
NPM_XENLA (P07222) NUCLEOPHOSMIN (NPM) (NUCLEOLAR PHOSPHOPR	46	9e-04

Comments:

TaqMan Primer/Probe Sets:
5'start=1007
5'stop=1032
3'start=1084
3'stop=1105
5'primer=AAACTAAGAAGAAACAACCCAAGAAA (residues 1007 to 1032 of SEQ ID NO:106)
Tm5=57.02
3'primer=TCAACATGTTGTCGTGATTGGT (residues 1084 to 1105 of SEQ ID NO:106)
Tm3=57.44
probe1=CACTTCCACCTATCAGCA (residues 1064 to 1081 of SEQ ID NO:106)
probe1start=1064
probe1Stop=1081
direction1=Reverse
Tm1=68.99
score1=1.99
length=99

CT1072
Nucleotide
Genomic coordinates:
Start: 255074
Stop: 257477(SEQ ID NO: 108)

Amino Acid
MLSFNPEYASWFGKMITDPGVILPVSKDVVLFGSRGQSDVGIMTLDPHDLDIKITSKRIG
VEERLAQYNTLPMDFTRAMEKELNNSRNMKESIFTGIFLDTGSAIFEDNMFNGGGSALRL
IRSPALNSAVFSSKNYIIKQLPTITKSLRRSQARDKQVDKTREKIVVDSFSILSAIAAQV
MHLTDGEMTYVPDGHCVNVVMSETNASSIYLIINDPTGSGWKIMPNNFNKTLEMRDGVID
RVETLVEFACKCVASSLIKRGMDLVDMQRTIRSMDFLPPASSTSNNTPRVAIMTSGSSTT
TGIGSLSILAEDGSTHHQIKLSEYRTGLSITENNREVSFTVEPSIDGVQAEHPLSPSILQ
WLPPLVKRPEVVAAAAAAVVEEENGDNKPSDKDNEDKYSDTDFWSNVPVTPLITPKKWRA
CKINDRAMISSWKNNLVKLHKYDWTNKTTKVDYFDKMAAFVALMTFRKFQDILADNYVPP
QTPSQGSEYAVTMSNVATLFTDVYGFESNGNKPLFALEQLENETGIESIYVLNIIGNSPD
GNSVRVVRLEKEMSFLLKAKQYFTEMAIPPINEKCKWTDKAPSSVKEYKYFCDLTAPISK
RPRKDNNDGGVEHSALTYTPRCIYHTERCLVHLYSEPEKITEHVSFNKDLNILEIGKNIT
NQYQTNYKSIFEIVDVPIIVASMSSTKTMTVNNYIISTPSATTKFVQDPPKTGKQLLAVE
EVRNFKLKSVLVPPPYFRDNKRNTTLCSQITEQNCPSSSEGGRFSCPSESLILKYSNLSK
KRALEEIAPETETSILSLAM
(SEQ ID NO: 109)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
TFC3_YEAST (P34111) TRANSCRIPTION FACTOR TAU 138 KD SUBUNIT	39	0.12
Q9XIC1 (Q9XIC1) F13F21.2 PROTEIN	38	0.20
P95629 (P95629) PUTA GENE	37	0.60
Q9XGN1 (Q9XGN1) TTG1 PROTEIN	35	2.3
O85475 (O85475) CELL DIVISION PROTEIN	34	3.0
Q00741 (Q00741) TAMA	34	4.0

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 1 to 932 of CT1072: this corresponds to nucleotides 256520 to 257451 of the genomic reference sequence.

TaqMan Primer/Probe Sets:
5'start=1048
5'stop=1068
3'start=1099
3'stop=1120
5'primer=GCAGAGCATCCTCTATCCCCT (residues 1048 to1068 of SEQ ID NO:108)
Tm5=58.38
3'primer=CTGCTACCACTTCTGGCCTTTT (residues 1099 to 1120 of SEQ ID NO:108)
Tm3=58.57
probe1=TTCAGTGGTTACCTCCTC (residues 1076 to 1093 of SEQ ID NO:108)
probe1start=1076
probe1Stop=1093
direction1=Forward
Tm1=69.00
score1=1.99
length=73

CT1073
Nucleotide
Genomic coordinates:
Start: 257551
Stop: 259132(SEQ ID NO: 110)

Amino Acid
MGVQKNILVGGGGGVSLLLGVVTLLGTVTEGAPAVPPFSSSSYSFTPESSVFWVEGNRVL
SGTKKDTLINVLGKKIPYYANSIFRHDCSETRSIQWPETSPLGLNLIFCSCASHEHQHRT
HETTEPDDLLWDGSRKTTTIILPKKWWSDVVWTSLWRDNDQKCGCGQAFVSSFTSTQKEV
QGEWLAAHTNGKTSEGDTNSAYLFISLQRTTLKPIITDVTEDNMMMGRMSGTPMNPKDMT
YFVNDFSDDIGSTPQCLVSNSDILNKREEWIAVWGVADSKDLLTKHQLGEREYGSEGRRR
NPGVEEEEEERVEEEEEVEVALPYIKKSGKLIGPRRRPLTTTTTTTTTTTNPIVREVVE
DFDYESFNEPEIFGSNSKLPFIRFLDQKNWRLGIMSRVSSSIANFKIEQESSKALFCLAV
WVGDEHTPKFRLSVWKNWKPFTSAPIIVQNVGYSSDVFWHETLRSKIVDRSRDLIETKVT
KKIGEDWANKKQTVVAMFISGIVCITVTVISIFSIVIYYKIKMPKF
(SEQ ID NO: 111)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
G1184543 (G1184543) NAD+:PROTEIN(ADP-RIBOSYL)-TRANSFERASE,	44	0.003
O17412 (O17412) CHITINASE	41	0.015
AAF00095 (AAF00095) HISTONE ACETYLTRANSFERASE MORF	39	0.10
AAF00100 (AAF00100) HISTONE ACETYLTRANSFERASE MORF BETA	39	0.10
O15087 (O15087) KIAA0383 (FRAGMENT)	39	0.10
AAF00099 (AAF00099) HISTONE ACETYLTRANSFERASE MORF ALPHA	39	0.10

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 511 to 925 of CT1073: this corresponds to nucleotides 258607 to 259021 of the genomic reference sequence.

TaqMan Primer/Probe Sets:
5'start=698
5'stop=721
3'start=823
3'stop=846
5'primer=CCATGAACCCTAAGGATATGACAT (residues 698 to 721 of SEQ ID NO:110)
Tm5=57.04
3'primer=GAGGTCTTTAGAGTCTGCAACACC (residues 823 to 846 of SEQ ID NO:110)
Tm3=57.29
probe1=TTCGGACATCCTGAACAA (residues 780 to 797 of SEQ ID NO:110)
probelstart=780
probelStop=797
direction1=Forward
Tm1=69.00
score1=1.99
length=149

CT1074
Nucleotide
Genomic coordinates:
Start: 274526
Stop: 275153(SEQ ID NO: 112)

Amino Acid
MYIFVEGSPLTGKSSWMSKLIDTGSCGMSFLNFLRMNTSDYYNWPAEIGTEHLQLGFRET
RVVDGMFEPVLKTFVDSWKKEQGKESLKEYLDYNGQVMEIYIAEWLRQRPLAFHVFTYTD
EAVKSGFLNEEDLDMDTATKWMAEIIREKRGNIQEIKVTPRVVFNGNVCSACFSNTKRNL
YNFGTNYNNVVHCDLLCPFARHRIVHFL
(SEQ ID NO: 113)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
Q9Y7X6 (Q9Y7X6) HYPOTHETICAL 75.7 KD PROTEIN	38	0.079
Q9YBC0 (Q9YBC0) 431AA LONG HYPOTHETICAL PYRUVATE DEHYDROGEN	35	0.52
O67329 (O67329) DIHYDROOROTATE DEHYDROGENASE ELECTRON TRANS	33	1.5
DPO1_BORBU (O51498) DNA POLYMERASE I (EC 2.7.7.7) (POL I)	32	4.5
YHC3_YEAST (P38742) HYPOTHETICAL 130.0 KD PROTEIN IN SNF6-S	32	4.5
O51342 (O51342) ATP-DEPENDENT CLP PROTEASE, SUBUNIT A (CLPA	31	5.9

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 1 to 563 of CT1074: this corresponds to nucleotides 274555 to 275117 of the genomic reference sequence.

CT1075
Nucleotide
Genomic coordinates:
Start: 277704
Stop: 278079(SEQ ID NO: 114)

Amino Acid
MWRSCISNIREMGDNKDYETRLIQRINDLESEIENKTELCEKINEQMKNTQLKYDKCFVE
EETEKFRKMEERVKYLKEQGIPLDPEERRTMLAEIDKSNKELDALLEENERIIKLIDEEL
ESMK
(SEQ ID NO: 115)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
O44929 (O44929) MICROTUBULE BINDING PROTEIN D-CLIP-190	47	5e-05
Q13439 (Q13439) TRANS-GOLGI P230 (256 KD GOLGIN) (GOLGIN-24	43	7e-04
Q59037 (Q59037) HYPOTHETICAL PROTEIN MJ1643	43	0.001
Q25662 (Q25662) REPEAT ORGANELLAR PROTEIN	43	0.001
KINH_DROME (P17210) KINESIN HEAVY CHAIN	42	0.002
AAD29948 (AAD29948) MYOSIN HEAVY CHAIN	41	0.002

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 388 to 1 of CT1075: this corresponds to nucleotides 277689 to 278076 of the genomic reference sequence.

CT1076
Nucleotide
Genomic coordinates:
Start: 278221
Stop: 278473(SEQ ID NO: 116)

Amino Acid
MQKKYDKLFEDDKRFREIEERILQQKEKGNPLDPEERLVLSADIDRSMKEIDDCLEEINH
IELSIDTLLDECENLHYGLQTTK
(SEQ ID NO: 117)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
O18164 (O18164) Y6B3B.1 PROTEIN	35	0.076
P70388 (P70388) RAD50 HOMOLOG (S. CEREVISIAE)	35	0.10
Q06268 (Q06268) INTERMEDIATE FILAMENT PROTEIN	33	0.30
USO1_YEAST (P25386) INTRACELLULAR PROTEIN TRANSPORT PROTEIN	33	0.39
Q07380 (Q07380) HYPOTHETICAL 206.5 KD PROTEIN YDL058W	33	0.39
O96275 (O96275) RESA-H3 ANTIGEN	32	0.51

Comments:
Hit to public SBV sequence:
gi|6007410|gb|AF178573.1: CT nucleotides 13 to 252 match nucleotides 2050 to 2289 of the public sequence with a 100% homology, a score of 476 and an Evalue of 1e-137

TaqMan Primer/Probe Sets:
5'start=88
5'stop=111
3'start=147
3'stop=170
5'primer=AACCCTCTAGACCCAGAAGAAAGA (residues 88 to 111 of SEQ ID NO:116)
Tm5=57.69
3'primer=TCCTCGAGACAATCATCAATCTCT (residues 147 to 170 of SEQ ID NO:116)
Tm3=57.97
probe1=TATTGTCGGCTGATATTG (residues 116 to 133 of SEQ ID NO:116)
probe1start=116
probe1Stop=133
direction1=Forward
Tm1=68.98
score1=1.88
length=83

CT1077
Nucleotide
Genomic coordinates:
Start: 278723
Stop: 280976(SEQ ID NO: 118)

Amino Acid
MEKKTETAATTEKDPEPSVSKRSRNKEPKTTSTVYTSVKCYLSSIIKSESSRSNVTSTKE
RFEERCKSVSKMMVKGSLFLRLVVDECLRRYNHLEDEIDKWPDMTKDNFYVQLLRKGLDK
KKLKEGSTHPVVEDVWNSPIVQETFLSQQGEGNNPIKRHLMDFNTITYAAKQLKTCFETN
LRTHFRTRQQRAISGWLAENGFDKKYTKLVQHWIIGCTYKSDWVDSGDLERVKEGTKNFV
TLHRKHLCVISDKKNGTISYSPEEKYPIPSILNYYKFLQTEYPQNKKIQKMIVVPKHKLK
IHYCTFDQTTIQGICKDLGVWKDMEERHKQSEDILYKQGWYLLFDVKKIKKLRPNWNFHS
IQTDGEGVSVLFSREVEEVETVSKKSKKNKKPRGDEDRRNYPPTNAKYVVGVDPGRTNVV
SCSVFDTRQKRVVRKHRMTAKQYYQESWMTDRRKANETYKKNNKEYKEALEEITRYDNGE
EIINDGNGDTSTPTKKFEAYLKVVNEHYRLLWNEKGKKKYRKNAMKVYSRKQKCISNFID
ELIPKRDKIEDYHIAFGDAKFACTGRGEQYASPARIFAKKIKERVGGDKRFTFVDEKYTS
KVCHRCNQPLNMLEKDCFSPNKKRKPPTIVTTTTTTTTEEDEENGKWKKATPLRENRDTR
RCSSEKTQFGYSSNRKVSTGDISMETPVPSSTSSSFCTPTSITCVLGGKFVDRDFNASTN
IVHKFLGFWDKKLMEKKDKMPLKYHFIRVA
(SEQ ID NO: 119)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
Q9ZAY5 (Q9ZAY5) SURFACE PROTEIN C	46	7e-04
CYL1_HUMAN (P35663) CYLICIN I (MULTIPLE-BAND POLYPEPTIDE I)	41	0.022
O62231 (O62231) F35E2.9 PROTEIN	39	0.086
Q12080 (Q12080) P2610	39	0.11
MYS2_DICDI (P08799) MYOSIN II HEAVY CHAIN, NON MUSCLE	39	0.15
O69188 (O69188) C3-BINDING PROTEIN	38	0.33

Comments:
Hit to public SBV sequence:
gi|6007410|gb|AF178573.1: CT nucleotides 12 to 297 match nucleotides 2549 to 2833 of the public sequence with a 99% homology, a score of 551 and an Evalue of 1e-159

CT1078
Nucleotide
Genomic coordinates:
Start: 282175
Stop: 282586 (SEQ ID NO: 120)

Amino Acid
MGNSESRSSGIEIVHKNGAPKRSHKTLYLSNRTERHAQIQKQIEELHHKTNKQFEQAQKV
LDKNEERKKHQQQQQIIIPLDPEERRAILAEIDKHMKEIDGFIEESERLGLLVDAEINNL
EEKEVEEEHLLKQKED
(SEQ ID NO: 121)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
ARP4_STRPY (P13050) IGA RECEPTOR PRECURSOR	45	2e-04
AAF05247 (AAF05247) ORF133	43	6e-04
MYSG_CHICK (P10587) MYOSIN HEAVY CHAIN, GIZZARD SMOOTH MUSC	43	8e-04
AAD46501 (AAD46501) LATENT NUCLEAR ANTIGEN	43	0.001
O40947 (O40947) ORF 73	43	0.001
Q9ZGM5 (Q9ZGM5) M-LIKE PROTEIN (FRAGMENT)	42	0.001

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 5 to 344 of CT1078: this corresponds to nucleotides 282190 to 282529 of the genomic reference sequence.

CT1079
Nucleotide
Genomic coordinates:
Start: 286863
Stop: 289635(SEQ ID NO: 122)

Amino Acid
MSSSSSSSFSFRISTYQTFLKALAHPDLVDKITQKCDETGRNQKCPIQFLADISHLIQGE
RNGGNLFPLHPFKNQPHLEPRIVGSLHGRTLDNDIEESYCYFVKDLYNGVFSYVNGVKEL
QGVLDKKISGSGSGESSSSRAPLIPITDVDLLYIFGTLVVLPPRSKAYRVITEAVLALPF
NEFSNNWPPTNIKGAYVSRDFRMFNLLAGLDHIEGEVGGESEWESIHASVVKRMVTIMRN
KAEKKPPSTSRIFRVYVAEPVNDAVTKIPIRVLSKLFGSRLAGILQKVYSYSMLNLPYLL
SSNSIDIKQGVKGITLSIPSARKLGFYLLQKDTTLQSSLSQDVADCIVSINAGIIGDDFS
EKIRQCIEEKNKPENCCMCFCEIDKTPDFSYSEHVARHNFFPVHAFSSSHDDKCCGAKIC
SECIFPYIISLYEKMTGVAGVKVVDLFQCPGCKSGMLNLKGRCYEFSNLCKRMILPYTST
HCSSLFDATINRAEACFYSLEFLQYDFETARRIAHGAKDIPHVYNKVVKNVKDLDRLCAL
YCYKCVSPVVCDEPNESTDYEMVDVTPPLINLTEIVDSEEYDDGPGNHMWPAKFTCNFIA
GSSGETPTISTCRDAVTFLGRAPRKKMAGWDDQSAVGQAIIALANWRKSGELPKNMFDLL
EGVNAVLYRGDSFLLRAINYPCVIGRSMSPSLELVKRKVNKIALIKAFFHEKRVRPDASK
KLLEWAELLVKSYLMEVLLQTPECVIHRAHSFVGKTLLITDELVHMRPDDATRNAYIQNL
NAARQNAAAAASFSGSLPKPEFVPCKERTIEWMYEKDNDDVRVVNCPSCKKAIQKYGGCV
NVFCECGTNMCWICEEKVSPADSNHCVEKHRIVYSNCVRVKYALESMYGFEICTMKNVEE
GVKNYYVMENGFFFDVQEMVAKK
(SEQ ID NO: 123)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
AAF04637 (AAF04637) HYPOTHETICAL 84.4 KD PROTEIN	213	3e-54
O97226 (O97226) PFC0175W PROTEIN	49	1e-04
Q94981 (Q94981) ARI PROTEIN	48	4e-04
CAB45785 (CAB45785) HYPOTHETICAL 262.6 KD PROTEIN	46	0.001
CAB36714 (CAB36714) HYPOTHETICAL 68.5 KD PROTEIN	45	0.002
Q9XII0 (Q9XII0) F7H1.11 PROTEIN	45	0.003

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 1 to 910 of CT1079: this corresponds to nucleotides 288641 to 289550 of the genomic reference sequence.

TaqMan Primer/Probe Sets:
5'start=1148
5'stop=1167
3'start=1192
3'stop=1211
5'primer=TTGACAAGACGCCCGATTTT (residues 1148 to 1167 of SEQ ID NO:122)
Tm5=59.14
3'primer=TGGACGGGGAAGAAATTGTG (residues 1192 to 1211 of SEQ ID NO:122)
Tm3=59.35
probe1=AGTGAACATGTGGCAAGG (residues 1174 to 1191 of SEQ ID NO:122)
probe1start=1174
probe1Stop=1191
direction1=Forward
Tm1=69.00
score1=1.99
length=64

CT510
Nucleotide
Genomic coordinates:
Start: 38917
Stop: 37381(SEQ ID NO: 124)

Amino Acid
MAETVAVDEVPTCPICMGDYDSDTDCYNWSNGGMPCCRKSVHLECLFTWRFEEHMVNENH
LLCPMCRAYIPPVWFFRKVYEEVYKYASFHSFLLSADYVNDEGVKDTLNKMSTILAPTFF
VPNAKGVNENEDVYMERAYTKLSFMLETLSRQEMHAFSEETFEDNHEAALMGKFKDIPPY
EYEGEWLKYVAPNTIDITQCLSNDDDDDEGDNNVSPSLLSGVTSFNFIEDDEDTVVFVPP
EVDDNDDSESLPDLTVPPRSNNITFDTISGISSSLYDVNDDDDDDDTMSLPDLNMPSAST
SSAPTSSAPTSTSLNINVNLCFNVDSDSDDEEVIPSSSSVNQPSTSSGSSSSSSNSRKRP
RYGRDEDRMSNISSESKRLCVDVKRYMCRLDNIDEEYNEIANRYLAELSALRERRQETEN
KLGDCISRGNLFHTTVNDVIGKSLCSKKLKVKRKYASKWSANKQLIGSCLIKSASNNARL
DDEIAHVHSSLLNGFDTDPSEADQISSLPNL
(SEQ ID NO: 125)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
O70567 (O70567) DENTIN SIALOPHOSPHOPROTEIN PRECURSOR	56	7e-07
P97399 (P97399) DENTIN SIALOPHOSPHOPROTEIN PRECURSOR	56	7e-07
SR40_YEAST (P32583) SUPPRESSOR PROTEIN SRP40	53	4e-06
O95815 (O95815) DENTIN PHOSPHORYN (FRAGMENT)	53	6e-06
P87736 (P87736) RING-FINGER PROTEIN (FRAGMENT)	51	2e-05
Q53653 (Q53653) CLUMPING FACTOR	51	2e-05

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 1 to 444 of CT510: this corresponds to nucleotides 37411 to 37854 of the genomic reference sequence.

CT511
Nucleotide
Genomic coordinates:
Start: 40718
Stop: 38972(SEQ ID NO: 126)

Amino Acid
MGGPTVITTTINTGGDHHHQQYVYHQGNKKRPVEEYNNNNYASGSTSEATTVPAYNNNNN
NITIKTWDDVINLSITPPPPKRFKKSEVAPSPPTTRTFSNVCASKVIRQCKRQYNEWIER
DSPYYFKGIEKSCSLEDNYDTCQQLRIGHRSIVKSSKYVHDTCFYGKDPKVGFYWPTSSC
DEEMRFFDTRHILKELSSRNIPSSQIMDIMYMAVEVFQLPSSACERIRQKTSTLIKEVSD
QCENWENFRKTARGCLSDLVEVPEDVKDFNTFICPWETFFEIKYGVYYIVNRGTVVKFMK
DMNYEEFVFECVNGLSVYRKNIKGVVGVTGVCPQGLCLEMPFAGISIDDVIRCVKDSLDG
GEYYESRDARLLYGVVMLQRMGRLPEVKGVDTVAPITDSFIARKVVRSMFEKLKVNMPFV
LAETCNVITRVANEGIINVDIKADNFVIDSISGQPKMIDLGLSYPLGYCYNDEYFRNTEE
LIRQYIHTPPEFFRGHCLGAYSMTYSFSVMASSILEDVVACSNMEGPAFNLMSNMHFLML
LQSGTDTDFYQNRPSITEYALAMKHIFPFKGTVMNLFKVKK
(SEQ ID NO: 127)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
Q15208 (Q15208) NDR PROTEIN KINASE	41	0.017
Q56921 (Q56921) PROTEIN KINASE A	41	0.017
O85239 (O85239) PROTEIN KINASE YOPO	41	0.017
O68717 (O68717) PROTEIN KINASE A HOMOLOG	41	0.022
CAB54949 (CAB54949) PUTATIVE TARGETED EFFECTOR PROTEIN KINA	41	0.022
YPKA_YERPS (Q05608) PROTEIN KINASE YPKA PRECURSOR (EC 2.7.1	41	0.022

Comments:

TaqMan Primer/Probe Sets:
5'start=878
5'stop=902
3'start=981
3'stop=1001
5'primer=GGACTGTTGTCAAGTTTATGAAGGA (residues 878 to 902 of SEQ ID NO:126)
Tm5=57.47
3'primer=TGAGGACACACACCAGTCACC (residues 981 to 1001 of SEQ ID NO:126)
Tm3=57.98
probe1=TGAGTGTGTTAATGGCCT (residues 927 to 944 of SEQ ID NO:126)
probe1start=927
probe1Stop=944
direction1=Reverse
Tm1=68.98
score1=1.98
length=124

CT512
Nucleotide
Genomic coordinates:
Start: 61872
Stop: 60672(SEQ ID NO: 128)

Amino Acid
MLSTCDLKHPSSTDGNVLKNIHFSESIPANDIISFPSSDTEELNKDLLDSVRNQIKFGFD
PITETLKNCITTQTLLHSFLKSSLLTLQEKFNEWGSIQLEKGGQEMALCASLKIMGQISA
LIETAKEASMDNKKKNNNACANCRDSKCSASLVTLFNKTIDEKYVKQNSSSASALLANTF
TAGANKPPKEFITKDNAHGNSDTNYTAMSDNLICPGKYYSSDITYEVTKQAKERIKNNNK
KMRLATGVEMVMKELEAENNKEGGRVEVEVEGVEQQQPSTSGEEMQMEIMLPTPPPPDLE
SLVTEGVDDYPVFSPLPSLLSPMPASPLPSNGNSALEDGGPFAPSADIVVDKTSEIMGRT
PGSEWVHQRDRNSKMEIRNYGARGSGINTGRYRRNNTVL
(SEQ ID NO: 129)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
GARP_PLAFF (P13816) GLUTAMIC ACID-RICH PROTEIN PRECURSOR	38	0.12
YMEI_YEAST (Q03433) HYPOTHETICAL 32.0 KD PROTEIN IN CAT2-AM	36	0.36
Q9WTU0 (Q9WTU0) PHD-FINGER PROTEIN	36	0.36
O15029 (O15029) KIAA0312 (UPSTREAM REGULATORY ELEMENT BINDI	36	0.36
MML3_MYCLE (O06081) PUTATIVE MEMBRANE PROTEIN MMPL3	36	0.47
Q06166 (Q06166) MATURE PARASITE-INFECTED ERYTHROCYTE SURFAC	36	0.61

Comments:

TaqMan Primer/Probe Sets:
5'start=549
5'stop=570
3'start=626
3'stop=649
5'primer=TGCAAATAAACCACCCAAAGAG (residues 549 to 570 of SEQ ID NO:128)
Tm5=57.79
3'primer=TGCCTGGACAAATAAGGTTATCAC (residues 626 to 649 of SEQ ID NO:128)
Tm3=58.13
probe1=GCACATGGCAATTCTGAT (residues 589 to 606 of SEQ ID NO:128)
probe1start=589
probe1Stop=606
direction1=Reverse
Tm1=68.99
score1=1.99
length=101

CT513
Nucleotide
Genomic coordinates:
Start: 77506
Stop: 76273(SEQ ID NO: 130)

Amino Acid
MEEHLSFNKPSPENGVVFFDFSDNTSMSNMVDNIRHRLPMDKKFSSKALLLASTPIPSDE
QLSTKVNKAIFSHRETIVLSKALKIVVTGLYVDGEYVDDVICLYPEKHTLNGILRYVVHL
NMMLMDKAEDADEIRCGLIPLGRGFNREAFKFVDPVIPCAGYNILNGYHPDNGHQISPSS
TQPQVQRRCAVKQMYKQINGMFEVVKQFSIKHNNRIFTINQVDFKGEEMKMFFALYSEEL
LPFYSETGKLLSEKHVSKSFSQLPPHVTISVFYLRNMEEYNTLMKTDFGSCFAPAIKIDT
GDNFELFGMNNNILVSKVCVGDDALDLRRRIMEHISDAIGRNVELADNRLNPHITHGKIN
EGVVGEWVSRFAPCNFLCKPREEIVFGGTKFIFGRVSNGNYVIKQPVDYV
(SEQ ID NO: 131)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
O32743 (O32743) RECOMBINASE	37	0.23
SYA_RHILV (P24075) ALANYL-TRNA SYNTHETASE (EC 6.1.1.7) (ALA	34	1.5
O03942 (O03942) LACTOBACILLUS BACTERIOPHAGE PHIG1E COMPLETE	34	2.6
Q9X257 (Q9X257) CONSERVED HYPOTHETICAL PROTEIN	32	5.8
O22993 (O22993) CELL DIVISION PROTEIN ISOLOG	32	9.9
YK05_MYCTU (Q10851) HYPOTHETICAL 30.9 KD PROTEIN RV2005C	32	9.9

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 1 to 982 of CT513: this corresponds to nucleotides 76314 to 77295 of the genomic reference sequence.

TaqMan Primer/Probe Sets:
5'start=502
5'stop=522
3'start=559
3'stop=578
5'primer=TACCACCCAGATAATGGCCAC (residues 502 to 522 of SEQ ID NO: 130)
Tm5=58.25
3'primer=TGCTTGACTGCGCATCTTCT (residues 559 to 578 of SEQ ID NO: 130)
Tm3=58.35
probe1=ATCTACTCAACCACAGGT (residues 537 to 554 of SEQ ID NO: 130)
probe1start=537
probe1Stop=554
direction1=Reverse
Tm1=69.03
score1=1.96
length=77

CT514
Nucleotide
Genomic coordinates:
Start: 102885
Stop: 100046(SEQ ID NO: 132)

Amino Acid
MDSTSTTTIEAEKALLKEYVNENLTWEFVDRVIRHEKLMQRTDMRLKTSSRRLFSFISIY
SFLQDFFTARDGVNSDEWCTQSALYHMLDGVASIISCFRKRIDYYNKKMERLACTSIREG
YFLVDVKTIESRHVELLDPDKKIWQRLYAEKIAPEKVVDAYNEVSKLLPDEAMANYNYRT
GLVHLSDTLKNAKKPPTDLTMTDFDFYEKYIRSDIVLGKSNKLSGMFSENFEILPDINIK
VPRRLERYFNVETNYSLEHNFRFPSNHIRGLIFAYFIGNIFGGAFSCVQLYLLGFTLSAA
SACRENVLDTPFSKLKQYIKNDNKTKNSSSNEDNDGEEYYPCELQYARINSNDKNACRKS
IVKAVKFVADRVEKASVTMMRTPIAEHESDGYMADWLSLQISKLLGRKVSASYALLFIVN
WVAHKYKQSFTNDVNGSEKYEILLKKLTVACGLTYNHKCGMVVPVIGFGSGMTNRKLRQY
AVHCIENVIGSFISSGKRKKDIHEDPKKLEEMSLMQLSARLFKNNDVMKRGQDGKVTFAN
EDNVQDFLEELKTKEFVPNERRRKIHEEEYTKSLHTNLKMTFRFGVCGFQHPLPASSDKP
TQVSLQLLKQRQTFVQRETAAAVNWTRLLQFLFPSDERDNKRHQNSLPWNRLGSNLNRHF
ISLASKFIKRSVHCERVVNDIISKFNADILPLGKDPDHFLMTKAGLVIEDHARENIDNAM
YSLCGGFNNQTTEQKLNSIRLRISAEALKNARNCVLATTFSKSYNEDRPFLPRTDEAKFV
PIPLFGVEPLHPLLNSFIDNTANKCNDSVSDFWLEESDDIFKEALVSHTILTDSSVYSTL
VGEDEDYCDNNKSGKRIGNTLVCTLYDMMGRANYNGLHSDKPRKHDPTPWSSKNTGQSGR
STTDFSPNSVIVLLDTENVADDYEDEEEDYEALKQSERDNVITLNNX
(SEQ ID NO: 133)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
Q12537 (Q12537) GLUCOAMYLASE PRECURSOR (EC 3.2.1.3) (GLUCAN	39	0.11
AMYG_ASPAK (P23176) GLUCOAMYLASE I PRECURSOR (EC 3.2.1.3) (	38	0.32
AMYG_ASPSH (P22832) GLUCOAMYLASE PRECURSOR (EC 3.2.1.3) (GL	38	0.42
MSH6_YEAST (Q03834) MUTS PROTEIN HOMOLOG 6	36	1.2
YMM1_CAEEL (P34489) HYPOTHETICAL 81.8 KD PROTEIN K01B6.1 IN	36	1.6
AMYG_ASPNG (P04064) GLUCOAMYLASE G1 AND G2 PRECURSOR (EC 3.	35	2.1

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 3 to 841 of CT514: this corresponds to nucleotides 99939 to 100777 of the genomic reference sequence.

TaqMan Proe Sets:
5'start=1126
5'stop=1147
3'start=1173
3'stop=1194
5'primer=TCCGTCACAATGATGAGGACAC (residues 1126 to 1147 of SEQ ID NO:132)
Tm5=59.41
3'primer=GGAGAGCCAGTCTGCCATGTAG (residues 1173 to 1194 of SEQ ID NO:132)
Tm3=59.86
probe1=CGAACACGAATCAGATGG(residues 1155 to 1172 of SEQ ID NO:132)
probe1start=1155
probe1Stop=1172
direction1=Forward
Tm1=69.00
score1=1.99
length=69

CT515
Nucleotide
Genomic coordinates:
Start: 114953
Stop: 110132(SEQ ID NO: 134)

Amino Acid
MSRNSLRVKGLKENGGIIPNPFDPLYVDTDAPFGMAGVKSDIIGKGFVESLLPGEISSHY
NTFDCFKTPKKCRVGGNDFECISCRSLGGGTCVKSSRELKTEYGIEDDDEYDGVCVPLAD
TIFSASSAFDKHDDDVATDAAYRNVNPFTTVEEAYLHYESGGVITGGGKKGTTYITKKRG
CVDSSVVRKDPSLLNKDPRLEPILGCTDIVLCGGKGVGRPIHPTTFSIIDDVDDIDFDIS
SMTSTMDCLCEPGYSQQRDPATNAPKCEKKEGGIQEKEQGLGCPVMFRYGVVGDTGTKGC
LCDESTQIRLEEVAGIDLPDAAKTDYAQPFVEGAKLLLQITERYETLGGSTKDACLPRPG
NDTRMSALGYSYAASLFGRAPEITAFNGGHLITGGLLRESAMDAAGNWHSRIEDSDEQGK
LTVSESVGGVVPYSGTGSVAAHIWNGDALNDNGLVGAGGGNFTEHPNASLRVVPLPHSNI
PGLGIDSIDHAVGIIASQGKIFPETVHMRAGDPSGVKTDRRDAHNDTTIETSFLKDSDKA
GYDSYKDNPLQKLRKSHDSGICATAYVVPSLHRVIKEKPSAKNDKTVNKILPLVHYRPTA
KRMAHTPIETIFKHSLLTAQERDQSFANSTLNSMMVTNSSNSFDDVTNLLLDYFFPNLNG
EGKERSGLPINTRSIYNEPNNAKFKEIGGIILQPVTAQGAKKSSTFARFSEKILSTNSPK
IIDHYKAGSSAVFKKVGEKEAYEMFAHPPTAWRIASNEGTFFSGRGLNNGIEGTGMREAE
RVAKTLSKKPDIFAGAILTGDGVLMNGASSPLVRPMEIPASSLPEHTWFERRSPVNARGD
PGSADNLTAINNTYDRVTKGDIRAILNSTTDIKTSFNSYAPARPFSKPLAPPAGVSAAAQ
ATSFLGVLGGFPLPIPSSFLIQKSVQESVSNGTVGSMHGIVPLKFHEGDELWQQCEVKET
EGALNFIPPPMALFESLLRVRTLSSETFIRPELIPNRFRADWGLSPHTAGHYLNGVYSPP
CVREETGQSFGYPCSGALSQYTTMMVPKPLGPQSHSSLSKFSIKSYVEEQTRLLPANIGE
KSIFEMQDPNSKNIFDKIGELGEKENCNCTNGLFCPKVNGGGRNKTDPIAATPSRGNRHS
RFPLMTTLPKNDVHLSAALLRAQSGDARILNTIGETKTNGRKINLKAATENIWDISSNVM
LAPNKFCAMRRSTAYTPYSTRQEKVPAAVLDERKGTFDRNAELLGDVGMTDIVSNDILME
DYERLPGVPPAEAEIFHIIRDAAKTGQEGAKARRIVDFFESSHGVTASTFNVGTFSPYVE
GVKDIVSLYATPCFTDIDSPTISADSATINEGASIEPTDGSEVVVEVVNSNMEMLGGSTA
GSTKKRRLSISDYVDLEEDAEVFTINKQGKATENLRVRTSSSSKYVEGGQKDMVGFYEAS
KRVPRVMRRVHVLPVLTPYHGGFESCAPTAAQSACTRGVEITYADFMRPSDLSGTKTTLE
GVRVKGPEPFDDLSTLYFRSVGGPNLRKFAHHHHFGYEGLMSRYYYTREKTVSVSEGDLK
DRFPFVCQSDRGPFPPKRDGTIQPLALVDMGVLPEGALTRRTISME
(SEQ ID NO: 135)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
Q24341 (Q24341) LARGE FORKED PROTEIN	37	0.96
Q24340 (Q24340) SMALL FORKED PROTEIN	37	0.96
O13788 (O13788) HYPOTHETICAL 59.6 KD PROTEIN C17G6.10 IN CH	37	0.96
CHOD_STRSQ (P12676) CHOLESTEROL OXIDASE PRECURSOR (EC 1.1.3	37	1.3
HAGA_PORGI (Q51845) HEMAGGLUTININ A PRECURSOR	36	1.6
P94986 (P94986) HYPOTHETICAL 88.5 KD PROTEIN	35	3.7

Comments:

CT516
Nucleotide
Genomic coordinates:
Start: 118885
Stop: 115402(SEQ ID NO: 136)

Amino Acid
MKIVQNNFTPDERSGVIHIRKPAKIEKAVFGNIAAAIDDSAAVRKDPKKKRNLKNGLEPA
SKKLAKNIERISSEELKRVTDVQDPKLLHSIMKRTARQIGYDIGDDISPQSAPDRDGSSS
SSLLPIRMINIRTEELLEKGGKDTIVRIHILDGILPDNVPLPFKAEIKVDLVDEKYEGED
GGGSSDSGPSLFETFPEEVPAGWPPITNDPNAFSRNNGNKQQAVFKHVEVNSLADGITLS
TKGSIFNTGNRLKISIVTEDKNKTVLFDSQVTISSPIPKITEVFACRNVALMRLDMPKAI
NYDNVEYTPDTLNEKYVSDYPANFPRLSRQAEIASNLAAKLPRENQLSDINKPSVSFVYS
KTNTVNTPVLNKVLYNETLKNMEGNESEGYKILNATEITHLRNPSNPARTFICVSVPESE
IEAQWKMLGWIVGFKTSSDVLTTSSGYNIVFPASKVTQSDKLFSVISTDVNANTNKVVVH
NTPSRVGCFGSSVNFRVDAATAPDWPGPTNGPDFFSYQLRPCIILKTDNDNREPRITAVL
SSPATEYAGERTTSLLPRALNVSVGPLTEVRGGDIITPVQTALLGGEQPTFKAPAEPTKL
YAVFPVLDSHNGLVKASDNPFQPIHSITSRNKTTVLTVSDVIVNDDDDDVVLEDKSYHIT
VSDPVSGSILAKENVLSSRITSRPIFIDGARDDRVFSVKMEVFGGDDKGIQMPFTMDGHF
EGQFSDMSVPSNELAIWNDPSTFTAPVRDTPATDITNKGIVYCRTTLPPISNRGIRDPFM
KQTSLVPLPTSIPEWAFADYGGEIKYPRHIFISSIRTNDTTNIVNTDTQTEFSIENWLRE
QIDKEQERHRQLLPAPSEAYTQGEKVYAKMYMGDGVSEETLDQIVHTSNTTYVVDESGTK
KENLLVNKEDKKLAAILGKWGIVVFGANKYPDEPADRYTNWRNTGRLRAVGSYSQLRQPV
APLQTRLATWPSGDPVTRLADGQFLVRLDPRCGGIGSANGFYNNNGANNEFTSSLLFAIV
GNQDKVVSYAERVRFYMKIVARNEGKKHLKNDDGLVLVDRNSALHRRLWNRTTFDHDDIV
LCVKIPQNVMSKIEPGTSSGVLVDPLVFANVASSTDREEFYKKFIDTSSGPVVIDRASVT
SSYNISVPLNFYTTCGFIVG
(SEQ ID NO: 137)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
DNA2_YEAST (P38859) DNA REPLICATION HELICASE DNA2	37	0.68
O94534 (O94534) PUTATIVE SPINDLE POLE BODY-ASSOCIATING PROT	37	0.89
BAA84527 (BAA84527) ALP14	37	0.89
YGS4_YEAST (P46947) HYPOTHETICAL 30.5 KD PROTEIN IN SAE2-KE	36	1.5
O28907 (O28907) GTP-BINDING PROTEIN	36	2.0
Q49547 (Q49547) LMP3 PROTEIN	35	2.6

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 1 to 888 of CT516: this corresponds to nucleotides 115494 to 116381 of the genomic reference sequence.

TaqMan Primer/Probe Sets:
5'start=1869
5'stop=1892
3'start=1984
3'stop=2001
5'primer=CATTCACAGTATCACGTCAAGGAA (residues 1869 to 1892 of SEQ ID NO:136)
Tm5=57.80
3'primer=ACCAGACACGGGATCGGA (residues 1984 to 2001 of SEQ ID NO:136)
Tm3=58.39
probe1=AGCTACCACATCACAGTC (residues 1966 to 1983 of SEQ ID NO:136)
probe1start=1966
probe1Stop=1983
direction1=Forward
Tm1=69.00
score1=1.99
length=133

CT517
Nucleotide
Genomic coordinates:
Start: 180036
Stop: 179421(SEQ ID NO: 138)

Amino Acid
MEFGNLTNLDVAIIAILSIAIIALIVIMVIMIVFNTRVGRSVVANYDQMMRVPIQRRAKV
MSIRGERSYNTPLGKVAMKNGLSDKDMKDVSADLVISTVTAPRTDPAGTGAENSNMTLKI
LNNTGVDLLINDITVRPTVIAGNIKGNTMSNTYFSSKDIKSSSSKITLIDVCSKFEDGAA
FEATMNIGFTSKNVIDIKDEIKKK
(SEQ ID NO: 139)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
SCH9_YEAST (P11792) CAMP-DEPENDENT PROTEIN KINASE SCH9 (EC	35	0.45
O39292 (O39292) COUNTERPART OF HSV-1 GENE UL10 AND VZV GENE	33	1.7
HS78_YEAST (P32589) HEAT SHOCK PROTEIN HOMOLOG SSE1	32	2.3
G435756 (G435756) LYSOSOMAL MEMBRANE GLYCOPROTEIN LAMP-2 HO	32	3.0
LMP2_HUMAN (P13473) LYSOSOME-ASSOCIATED MEMBRANE GLYCOPROTE	31	5.1
AXO1_CHICK (P28685) AXONIN-1 PRECURSOR	31	6.7

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 711 to 1 of CT517: this corresponds to nucleotides 179367 to 180077 of the genomic reference sequence.

Hit to public sequence:
gi|6856160|gb|AF173992.1: CT nucleotides 1 to 615 match nucleotides 50 to 664 of the public sequence with a 100% homology, a score of 1219 and an Evalue of 0.0

TaqMan Primer/Probe Sets:
5'start=227
5'stop=247
3'start=294
3'stop=311
5'primer=TGGCCATGAAGAATGGTCTCT (residues 227 to 247 of SEQ ID NO:138)
Tm5=58.19
3'primer=GTCCTTGGGGCTGTGACG (residues 294 to 311 of SEQ ID NO:138)
Tm3=58.60
probe1=TGCTGATCTTGTCATCTC(residues 273 to 290 of SEQ ID NO:138)
probe1start=273
probe1Stop=290
direction1=Forward
Tm1=69.00
score1=1.99
length=85

CT518
Nucleotide
Genomic coordinates:
Start: 190743
Stop: 188172(SEQ ID NO: 140)

Amino Acid
MTESKDYVLALVAETKTDEKRLNYVSEGLVAAISNLQNTPEKQRKVVISSDVFGPTWFNK
TTEFFNSGLRLAKGHLSKDAVMRSVYRDIEGVREHIIDPSWRLTETAAEELCDFTFLKQA
PLLNLLNAFENIMDGVFRSAANLVLYSTRGDTNEPSWVIDSEMLANRNNSTVADLAMGRA
KRAIALFLGYTLCDILRWKQSIASRMKERGLDPFAAMPPHLEYGRAADMIEKRIKDFIEG
SFSDGVTVSEEDGQSYVVPTISTVLTNMVSVIQEGFYPPKVGSFHEALLGREIMVLLSAA
IDAEYRAVLSRTRNAKPNPLTTKLDKYVNNPHLQMPSESVTEREKEWVERERERIKTTDM
TAENLFRDHPYLPKAIDGILGPKRTPTALQALQREYKRCNKFNDIVSPETLEYFLVNNRQ
VMFSNYSVTRVLDPDSAARFSMYVLWNALFLCSGGLTQKTNSSAVKSRLILQVFLKDMHS
LFVCQRCESGFITKSLDTFTISLKEQSKPSMGEQELETYWKAVLDALGGGGGNNKGAENV
NGLGELMVEILSADSGLLRGGGLGGDIGFEGKMKQKREDEEVRNMHLVDKKGYVFEAAKY
VHVSKGFAALSFYLLYAAAATSNPSITNNFDRAVYLLLARWGDLKFPTHNLWGNVPTDEN
TSSLLSFASFWALRNAVRARRNVIDASNTSFVPGRPLPLLSAFSSKMLVDNMLKNNYVKV
ENVNREKLIWKAFREMQTESEIWKTSGSKAASDRNVKKAKQDLIRNASIGRLIVEPVGKT
PISSIALFRSMKRSRSEDLKMGSNNKYRLARDTKTATPRNPLSYTGKIVFSLDDLKNFSK
DSYTTMKVFPLTPLDG
(SEQ ID NO: 141)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
CAA22155 (CAA22155) HYPOTHETICAL 46.4 KD PROTEIN	37	0.49
O95517 (O95517) DJ1170K4.1 (NOVEL PROTEIN SIMILAR TO KIAA01	35	1.9
Q43688 (Q43688) GLYCIN-RICH PROTEIN (FRAGMENT)	34	4.3
YHO0_YEAST (P38800) HYPOTHETICAL 149.7 KD PROTEIN IN IRE1-K	34	5.6
P97572 (P97572) CALPAIN SMALL SUBUNIT (EC 3.4.22.17) (FRAGM	34	5.6
O48591 (O48591) GTL2 GENE	33	7.3

Comments:
EST confirmation of the predicted transcript:
Nucleotides 515 to 1 of CT518: this corresponds to nucleotides 188146 to 188660 of the genomic reference sequence.

TaqMan Primer/Probe Sets:
5'start=1308
5'stop=1327
3'start=1383
3'stop=1404
5'primer=AGCTGCCCGATTTTCAATGT (residues 1308 to 1327 of SEQ ID NO:140)
Tm5=58.26
3'primer=CCTGCTTTTCACTGCAGAGCTA (residues 1383 to 1404 of SEQ ID NO:140)
Tm3=58.54
probe1=TGTGCTATGGAATGCATT(residues 1329 to 1346 of SEQ ID NO:140)
probe1start=1329
probe1Stop=1346
direction1=Forward
Tm1=68.99
score1=1.88
length=97

CT1003
Nucleotide
Genomic coordinates:
Start: 23709
Stop: 24300(SEQ ID NO: 142)

Amino Acid
MDVSSYKSTIDYHNIEDMDDLQRATYKDRMETELVLEMAKKEGRYVRSLATMDELEVPEE
PATCYTCGYTFIRRRAPPPKRKSIFREPCAYPELLPDAPSPVRLEELVDVPEGASFFTYP
PYDDGSSTSSSQAECEDDYPPPYDPSENPQRSQVCDYCTTRQVLSSMTDHARANLIKNLK
REKKALGLGRRNNFSY
(SEQ ID NO: 143)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
VP40_EBV (P03234) CAPSID PROTEIN P40 (VIRION STRUCTURAL PRO	35	0.46
Q9Y4G2 (Q9Y4G2) KIAA0356 PROTEIN	34	1.0
O88508 (O88508) DNA CYTOSINE-5 METHYLTRANSFERASE 3A	33	1.8
Q9Y6K1 (Q9Y6K1) DNA CYTOSINE METHYLTRANSFERASE 3 ALPHA	33	1.8
Q23804 (Q23804) SPID PRECURSOR (FRAGMENT)	33	1.8
O88799 (O88799) ZONADHESIN	32	3.9

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 1 to 736 of CT1003: this corresponds to nucleotides 23688 to 24423 of the genomic reference sequence.

CT1004
Nucleotide
Genomic coordinates:
Start: 26630
Stop: 27257(SEQ ID NO: 144)

Amino Acid
MAPNSFQKFAPVIKTEKKEEERDEHDDPLRQIDFRDRKTLICLTANCVSRKRKAGSAHDR
VYKVLRYGNPYKYRRPNRTHRGLALSMDQGEVGTCLPLRPMEETEENPIDKCGVAFLYSN
YNEGDGMTHLYNDEEYIKKCKTIEGGTRTWVKKNRQEYFRQALETLMMSHSIKQYSNFIF
FKEDMEEGFVHKLHTFINMVHPKKVSVL
(SEQ ID NO: 145)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
Q9XX10 (Q9XX10) Y39A1A.22 PROTEIN	34	1.1
P70392 (P70392) RAS PROTEIN-SPECIFIC GUANINE NUCLEOTIDE-REL	32	2.5
O75381 (O75381) PEROXISOMAL MEMBRANE ANCHOR PROTEIN HSPEX14	32	4.4
Q40112 (Q40112) HYPOTHETICAL 28.4 KD PROTEIN	32	4.4
ECE1_CAVPO (P97739) ENDOTHELIN-CONVERTING ENZYME 1 (EC 3.4.	31	5.7
O70651 (O70651) GAG POLYPROTEIN	31	5.7

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 1 to 654 of CT1004: this corresponds to nucleotides 26601 to 27254 of the genomic reference sequence.

TaqMan Primer/Probe Sets:
5'start=248
5'stop=266
3'start=291
3'stop=309
5'primer=TGGCCCTCTCAATGGATCA (residues 248 to 266 of SEQ ID NO:144)
Tm5=58.53
3'primer=CTCTTCCATGGGTCGCAGA (residues 291 to 309 of SEQ ID NO:144)
Tm3=58.32
probe1=AAGTAGGAACATGCCTCC(residues 272 to 289 of SEQ ID NO:144)
probe1start=272
probe1Stop=289
direction1=Forward
Tm1=68.97
score1=1.97
length=62

CT1005
Nucleotide
Genomic coordinates:
Start: 31091
Stop: 31961(SEQ ID NO: 146)

Amino Acid
MEGEHQYLNLVREILERGVKKDDRTGTGTLSIFGPQMRFSLRDDTIPVLTTKKIFWRGVV
EELLWFIRGNTDAKELAKKKIHIWNANGSREFLDSRGLYDRAEGDLGPVYGFQWRHFGAE
YDTCSSDYTGKGIDQLANILKTLRENPDDRRMIMTAWNPMDLHLMALPPCHMTAQFYVAN
GELSCQLYQRSGDVGLGVPFNIASYSLLTHLMASMVGLKPGEFILTLGDAHIYNTHIEVL
KKQLCRVPRPFPKLRILMAPEKIEDFTIDMFYLEGYQPHSGNLQMKMAV
(SEQ ID NO: 147)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
TYSY_HUMAN (P04818) THYMIDYLATE SYNTHASE (EC 2.1.1.45) (TS)	410	e-114
TYSY_MOUSE (P07607) THYMIDYLATE SYNTHASE (EC 2.1.1.45) (TS)	407	e-113
TYSY_RAT (P45352) THYMIDYLATE SYNTHASE (EC 2.1.1.45) (TS)	406	e-112
Q89940 (Q89940) THYMIDYLATE SYNTHASE	390	e-108
P90463 (P90463) ORF 70	387	e-107
DRTS_TRYBB (Q27783) BIFUNCTIONAL DIHYDROFOLATE REDUCTASE-TH	381	e-105

Comments:

TaqMan Primer/Probe Sets:
5'start=424
5'stop=446
3'start=479
3'stop=501
5'primer=ACCCTGAGAGAAAATCCAGATGA (residues 424 to 446 of SEQ ID NO:146)
Tm5=57.82
3'primer=AAGAGCCATAAGGTGAAGATCCA (residues 479 to 501 of SEQ ID NO:146)
Tm3=57.91
probe1=ATGACGGCATGGAATCCT(residues 460 to 477 of SEQ ID NO:146)
probe1start=460
probe1Stop=477
direction1=Reverse
Tm1=68.98
score1=1.98
length=78

CT1006
Nucleotide
Genomic coordinates:
Start: 32124
Stop: 32802(SEQ ID NO: 148)

Amino Acid
MAFNFEDSTNLFANMDLTAGTTTDPTRPNIIFFESLLPNSGIEVMKRRLVRQGKCGNFEA
SGGAMSYFWLEDNAEDMENLNSGSHVKTNCLALFLQEFISNWIEETDRHGQYCTFPQYMD
GGDGSRGGYFTSLAMKWMARDVTFFVFVDRNNTVENAASIWMYQKLLAIGAKVVKVIVDN
ASNPMFSVCNACRCKYPGPVSYVIEGHGVGHSDLTCDEISGFFV
(SEQ ID NO: 149)

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 1 to 624 of CT1006: this corresponds to nucleotides 32182 to 32805 of the genomic reference sequence.

TaqMan Primer/Probe Sets:
5'start=268
5'stop=289
3'start=340
3'stop=361
5'primer=TGCTTGGCATTATTCCTTCAAG (residues 268 to 289 of SEQ ID NO:148)
Tm5=58.01
3'primer=CGTCCATGTATTGGGGAAAAGT (residues 340 to 361 of SEQ ID NO:148)
Tm3=58.72
probe1=CGACATGGACAGTACTGT (residues 322 to 339 of SEQ ID NO:148)
probe1start=322
probe1Stop=339
direction1=Forward
Tm1=69.04
score1=1.95
length=94

CT1007
Nucleotide
Genomic coordinates:
Start: 32947
Stop: 34216(SEQ ID NO: 150)

Amino Acid
MDSNTSILPPSKRPGLNLLQVLGIIITVALIASVSSFIFYRVGKRKYYPSSSSSSELSDV
DNGVEGGGGTTTTPTQPSPDGGDGYVDLSPQKKAELRTRVANVIFQEVSKDQGVAFRRAM
NDSTDKIMEETEARINNFSEPFREATVEREVFKDDTDKNFILSTLDLTEEQFKDIVMAEV
KNQLENFDYEDMTRLIFDNIPETDYLWTTHFDPKKYDTYSEKVLGFSDINSIERISSTFY
KGKKYEVTTGNVAVLVDFESETIKEKAGNSLIRNVEFIVVDEQTYKSFFPAFNQVFFSFK
VNKEKREVTVSINNGCVGIVANITPLTTPVGAASGHYIYGTSTAKEKTYLFVIDKYDTTE
FVCGLSNKSTPLMALNILFMSDTVFPSFDEAERPLTDAKAVEILGKRLGVGRYTNANIRN
TQ
(SEQ ID NO: 151)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
Q56711 (Q56711) HOOK-ASSOCIATED PROTEIN TYPE 3	39	0.045
O77363 (O77363) MAL3P4.5B PROTEIN	39	0.059
YLM5_CAEEL (P34379) HYPOTHETICAL 49.8 KD PROTEIN D2007.5 IN	37	0.23
GBA2_CAEEL (P22454) GUANINE NUCLEOTIDE-BINDING PROTEIN ALPH	36	0.51
Q9YW03 (Q9YW03) ORF MSV089 PUTATIVE NTPASE, RABBIT FIBROMA	36	0.51
P87199 (P87199) KINESIN MOTOR PROTEIN	36	0.51

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 1 to 907 of CT1007: this corresponds to nucleotides 33238 to 34144 of the genomic reference sequence.

TaqMan Primer/Probe Sets:
5'start=648
5'stop=674
3'start=773
3'stop=799
5'primer=TGACACGTACTCTGAAAAGGTATTAGG (residues 648 to 674 of SEQ ID NO:150)
Tm5=58.05
3'primer=CCTTCTCTTTTATTGTTTCAGATTCAA (residues 773 to 799 of SEQ ID NO:150)
Tm3=57.41
probe1=ATGTAGCTGTCCTCGTTG (residues 752 to 769 of SEQ ID NO:150)
probe1start=752
probe1Stop=769
direction1=Forward
Tm1=68.89
score1=1.89
length=152

CT1008
Nucleotide
Genomic coordinates:
Start: 34217
Stop: 35048 (SEQ ID NO: 152)

Amino Acid
MEGVILDKIETIAKRASPSYGSIDVGTAILRRQFMEKIRGKINEETTMEKIMGTKEERED
TIRSIVANVIKENTVKENVTEKIRAMTDKELNDNREFMHDFGKISTGDGGTFHLFEDTPG
FESALKAEYKNVPGATTPKYVSMNSLRIDAINGKIEEVYNPSPIMGIREYGTIRRGRYEE
NAGSKELVFMTKIEKRPNNVAENLIIRVANQQYNVMRMVFFIDYETKKGVSKEEMFIPYN
VQKTKALKGRSTYFSFVRKIPDEPEGSIIIHALGFY
(SEQ ID NO: 153)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
BAG_STRAG (P27951) IGA FC RECEPTOR PRECURSOR (BETA ANTIGEN)	41	0.007
Q99051 (Q99051) IMMUNOGLOBULIN ALPHA FC RECEPTOR PRECURSOR	41	0.007
YIBA_ECOLI (P24172) HYPOTHETICAL 31.8 KD PROTEIN IN RHSA-MT	38	0.079
Q46749 (Q46749) ORF-A1	38	0.079
Q25920 (Q25920) MATURE-PARASITE-INFECTED ERYTHROCYTE SURFAC	35	0.53
Q06166 (Q06166) MATURE PARASITE-INFECTED ERYTHROCYTE SURFAC	35	0.53

Comments:

TaqMan Primer/Probe Sets:
5'start=361
5'stop=384
3'start=429
3'stop=451
5'primer=TTTGAAAGTGCTTTAAAGGCAGAA (residues 361 to 384 of SEQ ID NO:152)
Tm5=58.35
3'primer=TCGCATCGATACGTAAACTGTTC (residues 429 to 451 of SEQ ID NO:152)
Tm3=57.96
probe1=CCAGGAGCAACTACTCCA (residues 397 to 414 of SEQ ID NO:152)
probe1start=397
probe1Stop=414
direction1=Reverse
Tm1=69.05
score1=1.94
length=91

CT1080
Nucleotide
Genomic coordinates:
Start: 291719
Stop: 292205(SEQ ID NO: 154)

Amino Acid
MTSPAPSPSSTPKSSCTTIVNRCGFLLDNNKEVVIYDTNSKFKCEPKNLELIGVLSGVSD
NVVTQISPDQIFVGTYMVKYNWSKSGHERFSDMSNNCLDNITRPSEVIESVIKKTSSDFK
MKYTRSLMDHTEKYYFSGDQKLSKISSWCTTPIRQWVCNSV
(SEQ ID NO: 155)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
CAB45519 (CAB45519) GIBBERELLIN 20-OXIDASE-ARABIDOPSIS THAL	32	3.0
Q52743 (Q52743) CELB	32	3.0
Q39110 (Q39110) GIBBERELLIN 20-OXIDASE	32	3.0
O60963 (O60963) L549.2	31	3.9
FLPA_ARCFU (O28192) FIBRILLARIN-LIKE PRE-RRNA PROCESSING PR	31	5.1
DPOE_YEAST (P21951) DNA POLYMERASE EPSILON, CATALYTIC SUBUN	31	6.7

Comments:

TaqMan Primer/Probe Sets:
5'start=201
5'stop=220
3'start=290
3'stop=312
5'primer=CCCCGACCAGATATTTGTGG (residues 201 to 220 of SEQ ID NO:154)
Tm5=58.70
3'primer=AGGGCGTGTAATATTGTCCAGAC (residues 290 to 312 of SEQ ID NO:154)
Tm3=58.09
probe1=CGCTTCAGTGACATGAGT (residues 265 to 282 of SEQ ID NO:154)
probe1start=265
probe1Stop=282
direction1=Reverse
Tm1=68.90
score1=1.90
length=112

CT1009
Nucleotide
Genomic coordinates:
Start: 35073
Stop: 35967(SEQ ID NO: 156)

Amino Acid
MALQEKDITIGNVSAALRELMYSPTHMQHHDKLNTFLDRNVESSSEEKIRQIVDKIRSQT
TSDISETVNNVTTNGTAFSLFEDTLEGMVKKNIGDNLQSGDFIDGRKKLNDMKSLATGAI
LSRQRDFVAESITGTKDWLKAIMGCGIIRYTVFVNNLARSTLDNDDDKAATYYNTPIYGG
YCKMAIKDYEIPDSYSKVEAEHTVEGRKMTFNIKWRGDTINNLITIIPSVTGYLASISED
ADVQAPLLLNCNNCFIEADMSSLYMDEKKTEASFTLNLPEIEGADANAVYEICIVVV
(SEQ ID NO: 157)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
YB75_YEAST (P38321) HYPOTHETICAL 101.2 KD PROTEIN IN FAT2-P	34	1.3
Q08281 (Q08281) CHROMOSOME XV READING FRAME ORF YOL138C	33	2.9
Q92271 (Q92271) 12.8 KBP FRAGMENT OF THE LEFT ARM OF CHROMO	33	2.9
Q26032 (Q26032) VARIANT-SPECIFIC SURFACE PROTEIN	32	3.8
O02179 (O02179) CALYX PROTEIN	31	8.6
O01394 (O01394) POLYHEDRAL CALYX PROTEIN	31	8.6

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 1 to 780 of CT1009: this corresponds to nucleotides 35166 to 35945 of the genomic reference sequence.

CT1081
Nucleotide
Genomic coordinates:
Start: 292189
Stop: 298777(SEQ ID NO: 158)

Amino Acid
MQLRLENFVKEEHETVVVHNPSGMTGFNIFNSSPVYFEVHNEMDALIFMAAFLKHNSLWG
EINANMDLYTFDYAGAFLDERWCHHEKSFSVVRAQLINSYYKCRRKIMQALDNNYNNKNK
KRKNVGGAPAFTFMSGDGEGGKEALEASFDVIGGTRGGRFGVDSTPCPHSSAMQLKLDNE
GNYGCIACFASMFFVLENPGDESSFISTDASKIGQAQAWIDERLRNNENGGEENNVFKKT
FHMLADITQKAHETAYSNTIPLGPNGRQWNWPTHTVEPIAHEFVTHSLVNTLKNLGDRKL
PRFNFDILYNLLNPFGKMLLVFIQNCHILTGHKNNENVVPRGSASGKWWTINFVGVNMWT
FQVTKCKVEKDRKISDLACMETLPRLPNPGSTTVDDRIVFKGFCRGENLGSVGEVVSDIT
QSVKNFCLMVENRKFSVDKETGFISSESIVSDPFFSLEVTGCRSNRAQDTINNGRVSARV
MRILKSREGARVWLAKDENAIIFENVNHDTAISTDAMERAIGQHKILYYDIETTDKDFTD
KKSVITSIGFCLCTGGDMTHGGERGVFGLVAPGSDVEKVKETIINSYDPEEKEDIMKQCP
QVIEIFTNEFEMLLGFGKYIDKVKPHVISGWNNVAFDDPFVFTRIVKHLSDHTKDMSYCV
ADASTAESVLPRATEGGGGGETPYRLSTPQERIQLASTGIFNKLGKFVDKKTGMLKPEMT
ADLLAGAESQANTKFKERNKLSSSNKGSAGWFQKIIGGMCSAIRLDLMKVCEKAYKESLS
EFNLNAVLAKVSSVGDKVKNVKDEVDLHFHLLGFLKLKKAQDQAKVHVYCCKDAYLTGIV
STSINKEGEIFRLCMDSALTEAVVTANLATPLCIGEGAICRNMGEERADRRGVGVRRHSI
ATDTKGGMVSQPIVNHVPYQTIDMTSLYPMTMCQNNLCTTTFVTHRQIMQLRDRLVLEKM
KNKTTDSLLLLDVIDECNQIVLSEYRPIDIAVASWKNSNSNRQTPITRIEESLGLRFIEN
LDAEKTNNKTWCTNTSPNMNVTAAGMDYFPEIVCDINMQFAAKVNDDMHIAPASLEYMLQ
VLPIMLIDRPYIGAHITAGKCRTLEDILSELEKDFSVEKDEEIIRTHWTFKGQKQYDFCH
SPVTQMARHIIESTGRNIRDYEGNEKFERLVSLSDRIYRRVGAFDSANDPAVRLWSSRLI
NVGMLVRTWNVKTDILKGIIPQMQATYRADRVVMQNKAKEFAKMGDMKRAGLNKVGQNIM
KLGMNSMYGHLALRARSSRKEFASGSANTASSISNMSATGGIGGGTRHSVTANQITENAR
CVFGNIGCGLQMALPGTKQTYGDTDSVFCVHNIVGDGGMIPEYDEQTGKYYYVMDIALKN
KMAAIIPILVNSLTKGIQFVERRDAGVGMMNIAHERLAVAGLLFAKKTYHMLHFNENSAA
FNDMIKLKSTDNNNKFASFIKRPSHADGYVVPHNPSLILRAAEGPAGKKLKSFLEEEGIH
DEKSMEEWFTSSPTWMAMDASVINNLYASQIVGVEKGNWIDAMTSRPIEAGTEMMEAVTQ
ANAAFTPYKKGAFVKKGITPTTKLKGLQSLIARFLPKIEEKKSCYLDVMKNHVENFASHI
TNPAMMITSSRVNKFDTSKEQSRPNPLALAINNHLNPSSEISLGQKFKTVTSVSSWSLSA
EEGEVPAGYFNAGSVRWDATNMKGSVPAFSVKNLSVVPNAITSVYKMVESDKTAIKSMIA
KNVEVLCSTSANTGFSLRRGALSFNTGVIVTKDVAMACIRSLNNKQMLLFVGGGKDYGED
DDDDDEEAEEEDEENGENEENKGDCVTEKKIPGRSTNKDVGEETKTSEKTEGERKGSKTA
KGKTEEIASSLSKCGKKDARDVILDRLLKATHSSCTNNEERTRVLQQYSNCTLSSYITSV
MKLDQRVADQMENLISQLDQIRNLSNKKRQEKGGPFKSELDAMVAAVKVKFFPVLDASRK
LTQDHWKKCPVSIPETREEKPLMGVPFEVALNSLIGKHKCTDTCDMACCQSLYFVLLYTL
ALKFENERLARQIGLDDSVDLMAEMLFGGDKLLAQEVLKRVKDAQDRKLVKSLLPLNYNH
DTNTIIFLFESLRFAQKPVAGMSVSEIKDAVRGLAFSTTTGTVWNYTDERFFGPLYNMDE
LCNERVNGNCKLSFITGIYHTAAVELAAACLSCVL
(SEQ ID NO: 159)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
DPOD_YEAST (P15436) DNA POLYMERASE DELTA LARGE CHAIN (EC 2.	52	5e-05
DPOD_SOYBN (O48901) DNA POLYMERASE DELTA CATALYTIC CHAIN (E	51	8e-05
DPOD_SCHPO (P30316) DNA POLYMERASE DELTA LARGE CHAIN (EC 2.	50	2e-04
CAB58156 (CAB58156) DNA POLYMERASE DELTA LARGE CHAIN	50	2e-04
UBF1_RAT (P25977) NUCLEOLAR TRANSCRIPTION FACTOR 1 (UPSTREA	50	2e-04
UBF1_HUMAN (P17480) NUCLEOLAR TRANSCRIPTION FACTOR 1 (UPSTR	49	4e-04

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 4 to 1205 of CT1081: this corresponds to nucleotides 297608 to 298809 of the genomic reference sequence.

TaqMan Primer/Probe Sets:
5'start=2738
5'stop=2760
3'start=2817
3'stop=2838
5'primer=TCGTCAATCATGTTCCCTATCAA (residues 2738 to 2760 of SEQ ID NO:158)
Tm5=58.05
3'primer=TCGATGGGTCACAAAGGTAGTG (residues 2817 to 2838 of SEQ ID NO:158)
Tm3=58.56
probe1=GATGACCATGTGTCAGAA (residues 2787 to 2804 of SEQ ID NO:158)
probe1start=2787
probe1Stop=2804
direction1=Reverse
Tm1=69.00
score1=1.99
length=101

CT1082
Nucleotide
Genomic coordinates:
Start: 300935
Stop: 305108 (SEQ ID NO: 160)

Amino Acid
MTEQGDQGIKVRKLHGPRGERGETGPAGAVGPAGPQGERGAIGPAGKDGAVGPAGPQGER
GAIGPAGKDGAVGPQGPPGERGENGRPGRDGAVGPQGERGAIGPAGKDGAVGPQGERGAI
GPAGKDGAVGPAGPQGERGENGRPGRDGAVGPAGPPGERGAIGPAGRDGAVGPAGPPGER
GATGIPGRDGVDGSVGPQGERGEIGRPGRDGAVGPAGPQGRRGATGRAGKDGAVGPAGPQ
GEKGEAGKDGSIGPQGIQGPRGETGPPGRDGTAAERGERGFPGPPGETGPPGKDGVDGSE
GPQGKRGETGPVGPRGEPGLAGLPGRDGAIGPAGPPGERGATGLPGRNGVDGSIGPQGRR
GATGRAGKDGAVGPAGPPGERGATGIPGRDGVDGSVGPPGERGETGPAGRDGSVGPAGPH
GERGENGRPGRDGATGPIGPAGPQGEKGENGRPGRDGATGPIGPRGETGAMGKNGVDGSM
GPQGRRGATGRAGKDGAVGPAGPPGERGETGPAGRDGSVGPAGPQGETGLTGSPGRDGAT
GPIGPAGPQGEKGENGRPGRDGATGPIGPAGPQGEKGENGRPGRDGATGPIGPAGPQGET
GLTGRPGRDGATGPIGPRGETGAMGKNGVDGSTGPQGRRGATGRAGKDGAVGPAGPPGER
GENGRPGRDGATGPIGPAGPQGETGLAGLPGRDGAIGPQGEKGENGRPGKDGATGPMGPP
GERGETGPIGPAGPQGATGLPGRDGVDGSVGPQGKRGLIGRTGRDGAIGPVGPAGPKGET
GLAGLPGIDGKDGSVGPQGAIGPIGPRGERGETGRPGRDGEDGSTGPMGPQGLRGATGAP
GPQGERGLKGRPGKDGETGPPGRQGRDGIMGPRGLRGEKGAPGNDGLEGPEGRDGAPGPA
GPIGPQGIRGLKGIQGRPGRDGEMGPAGKDGIEGPRGQDGTTGAKGPRGLRGFQGRTGET
GAQGSRGEKGDRGLTGPQGRDGPPGEEGPQGLRGERGAPGPRGPRGIRGRSGPQGSNGVQ
GPRGPRGTKGRTGIQGLTGIEGPRGPRGIQGKEGRMGKIGHRGEKGDKGDRGEQGIAGAD
GEKGPRGLRGIRGPIGAPGKPGTEGVRGPRGVRGVPGYPGAQGELGPQGPTGPQGPAGPQ
GPMGRTGDTGPMGPPGAVGPRGEKGGRGRKGKNGPKGADGKDAVNIIQKYSITHARAEIM
WEGNEIGEAYIGRSYGTDTIPVMIENRIGMTNEDKKNEYCIQVMTMHSITTRGRTSGVFV
VSNKTDYILLVTLLMPESVSCRTDVSTNARSERVNAVRERESKSYRFIRPSDQSIGTHSR
SKIAVVMYPDASMSYSVDTLDADVARRETTSVLLLAETIHGEKDRGFYADRGTVGRLMVP
PTEEELLVLQX
(SEQ ID NO: 161)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
Q14054 (Q14054) COLLAGEN TYPE VII PRECURSOR	940	0.0
CA11_CHICK (P02457) COLLAGEN ALPHA 1(I) CHAIN PRECURSOR	935	0.0
CA17_HUMAN (Q02388) COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (	933	0.0
Q63870 (Q63870) TYPE VII COLLAGEN	928	0.0
Q60444 (Q60444) TYPE VII COLLAGEN (FRAGMENT)	925	0.0
CA11_HUMAN (P02452) COLLAGEN ALPHA 1(I) CHAIN PRECURSOR	923	0.0

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 1 to 557 of CT1082: this corresponds to nucleotides 304552 to 305108 of the genomic reference sequence.

CT1083
Nucleotide
Genomic coordinates:
Start: 50094
Stop: 50295(SEQ ID NO: 162)

Amino Acid
MAVTEIPCGTRNIAEEDVELELILVTAEAEVREAMAAALAAAIIGAVVVQIGRVLDEVVA
AEVELM
(SEQ ID NO: 163)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
LIPB_MYCTU (Q10404) PROBABLE LIPOATE-PROTEIN LIGASE B (EC 6	30	1.8
Q64033 (Q64033) ANTIGEN LEC-A	29	3.1
OL56_STRAT (Q07017) OLEANDOMYCIN POLYKETIDE SYNTHASE, MODUL	29	5.2
RPSD_PSEFL (P52326) RNA POLYMERASE SIGMA FACTOR RPOD (SIGMA	28	6.9
O54540 (O54540) RNA POLYMERASE SIGMA FACTOR	28	6.9
Q9YAS2 (Q9YAS2) 136AA LONG HYPOTHETICAL PROTEIN	28	9.0

Comments:

TaqMan Primer/Probe Sets:
5'start=24
5'stop=45
3'start=95
3'stop=112
5'primer=TGGTACTCGGAACATTGCAGAA (residues 24 to 45 of SEQ ID NO:162)
Tm5=59.21
3'primer=CTGCTGCCATCGCCTCTC (residues 95 to 112 of SEQ ID NO:162)
Tm3=59.19
probe1=TTGTAACAGCAGAAGCAG (residues 71 to 88 of SEQ ID NO:162)
probe1start=71
probe1Stop=88
direction1=Reverse
Tm1=68.98
score1=1.92
length=89

CT600
Nucleotide
Genomic coordinates:
Start: 1118
Stop: 491(SEQ ID NO: 164)

Amino Acid
MHMWGVYAAILAGLTLILVVISIVVTNIELNKKLDKKDKDAYPVESEIINLTINGVARGN
HFNFVNGTLQTRNYGKVYVAGQGTSDSELVKKKGDIILTSLLGDGDHTLNVNKAESKELE
LYARVYNNTKRDITVDSVSLSPGLNATGREFSANKFVLYFKPTVLKKNRINTLVFGATFD
EDIDDTNRHYLLSMRFSPGNDLFKVGEK
(SEQ ID NO: 165)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
O51578 (O51578) EXODEOXYRIBONUCLEASE V, BETA CHAIN (RECB)	39	0.033
O68195 (O68195) DIOL DEHYDRATASE-REACTIVATING FACTOR LARGE	32	3.2
BACC_BACLI (O68008) BACITRACIN SYNTHETASE 3 (BA3) [INCLUDES	31	5.5
TKT_MYCPN (P75611) TRANSKETOLASE (EC 2.2.1.1) (TK)	31	5.5
Q9ZER8 (Q9ZER8) REPAC1 PROTEIN	31	7.2
CAA10001 (CAA10001) REPAC PROTEIN (FRAGMENT)	31	7.2

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 1 to 569 of CT600: this corresponds to nucleotides 513 to 1081 of the genomic reference sequence.

CT520
Nucleotide
Genomic coordinates:
Start: 209342
Stop: 196799(SEQ ID NO: 166)

Amino Acid
MFKANVLNLGGGKFLESDVRDHLIKCANQMKEEPTTLRICLSNKLPEYDNRRLPLLLLNE
GEQILVTDNLTKNGNPLVKQMGHLAVQDRVGGDGSVNPNNLLYAGCNVVEYDTVNRGNDG
KLIMYSQPATLKDVAKSKKKGMYKVKKVPEITGDQFLDKLNERSCQNENRRMDEEGPHVG
TGKLLRELIIMMRLYEEETSSAEKLCVTPAFREFLGCGRTATDVPVFKVAFITNASLMGL
KVIFYPTILEEERLAAVSDTENVVLLKSILKVQLELLSECMPRIVERVESMIKKTVACFK
IDIGGSDNWNLPGHCKVSDTAFPYHHAQLVGEKKNILSISNENMVTSLGVVKADRAEEWM
CKTLESFEKKCLYLENLMGSMANTDDWRRKILFSELGPEMPYRNKSLIMDQDFCTIGMCY
KFLAEGGGLLLTKTNATLLKEKMACKGLDDSGDGDDEEEDNEEGGSGGKSGGGSGDENNI
NKPPPAPKQIPPLAANVYNSIINDDDKLDQIVCFFKRKHGFFLSDIDNSPLLAMEFLLPQ
KAMSKKNCVERVKPETKNIIRNLTGVNTIKFDTIMPFAILQIVVRYENRNLKLPRDTDIL
QQRLKNNTWDALSKGKFAEMWQFTHKESLKPPTIEELESIPPPPTQSEEEAAAAAAASTS
STTPDMVSSLEEGATSTSSSDENQIASLENIKKLLSIITSTFATGADKNDTIFAWTVVTL
AERFCALYNITSHPEEYYQQIIREDFEFEGGFEKFRHMCDAINRELSIYVPKSVLEKQSV
CRMGVAAYENSMERIKNKTNSKLCKIKYDESTMVYELNNDTFKTFDYDESDKSFGPMYEC
APMETFQRLFASVKSDKEAVLADKKSEKREKLYQQKQEYLRKCDNDDVSARQILNNVASN
ESDEESDEESDDEENYGAAKGGATGDYYGGDDEDDCYGFLGEFGSSDDENVPSDNASSIN
NVQDDVFRDVNFIKTFNFRSSLCHRQKYVSTVIVEEMEKNLCDVLTLDNSAAESGDILKE
INRRSLRMRNWVVPFTMPVREIVKPNVNSEDGTANSNNNIPPFCSCASLNNFKSDSPLSS
NNTMSNEKCIKLLPIPSSKHLKDLTVALRFNTMACERRYFSDVTAALGFVKKDKVNGNIR
SILDNKRWDAIKQCKLAGKCLSSALPLGIYENVISEDNKLINTFRPRSLARLACSSGGDG
VSDKSVNNGFFSGIWALCANQDLESVVLGSTVVDPLKPTKVFNQSLSEKELKEKRQQMCL
DAANYFKDHNVSKLNIYECFKMMEECIMRTALNGKTSNDSEFFSNLITRYGSGTNSPASR
LWTILETVRECFNNSLPIDWGSLVKDWDGSDMLNLKAGVSNVDESGAVFELSEFLGVSAR
AFFGKDLDTNLDADTWECLLNDDNKDWKAQVAKAYEFALKDNDIRSVENFINSSNLLTNN
NVIKKLKIKPTPSNDVRHQIWVEDEYYPRNKSTLRSRAEWMAATEEVLKTEMSLSCVLAM
VAMYRIMMQGESVREIATAPLRLSVDKMVPLIRCFKITSKWCSCTGKGDSPKKADASIKE
GRFYDIEEDPLHFYRFAAYVIGQVASNDIVIEEMTRKILMSFDFNGFDTSNWLQFITYRF
SHVLMGRRSRLLSRPLSLVKNLVSVSSLADKNSEKSNDMYEKRVGKVMKRIARLVLVKAA
DSVRASSNDLLDCCILDVNDVSVKSLDEFRAKTRQELQETRIDTNYNLVSNSCTTAQLAA
VEKSSRIINTNISFHNIPAGQAKVMDANEEAFIDPSLEEINKEDNSGAKQMTGKGGSNRG
RSKKSGGGGFNNAGGFYNDDSSRGSSSVVDEDSRSRTGFSQIHMDARNEEDRESGLFSYD
GYVLNRIKNMITQNQINNDIVKVISDIENFFKICVPFSKKEYALYGVTETALSAGMDAIE
RWNKAVEEETNKIRKECRDLTDTGSVYDMNIICPGDYMSSVGEGGNGGCGGGSSSSGHLL
SNNNNEANQTNEISEDQLKHEGSDCSFWFNFYKKVVNSSEKKQGKGSVLANTGHEGRIVG
RPLRTFIQYKGKGFAETKVLTRYFSNHISDSYWSQVMPICYIKNMALGDEDKSKKKFGKR
PWKNFNNNSNSSSNSSVKYVSIQDLEKKDSLKNVPMGYDEDLLSLYDDSLTTSTEKLENI
KIVNDSKDAYVILGSSNQSSFDQTFSQQYFTHQKISNINTYKSLGKMWNCNNGMSPKNQI
VLLKKLLFKNLNILWIKLYERHISVLCNWGCIHPNSSKNSHFEMTKNNAPCGVTDSNPPL
SVYHSGFLSVEDYGQLLKDTFPLMNLHRTFSAKSKDNNSSDPSPEKISAASLAKAVYARE
VLSSCLDPEGNFCTSWITNSCSVLFTPGTNIRRGGDFFNKSCYRQQDNDYCFIGKEETKK
CPNFVSSEIEIVSILKTAVFLSTNSDGHKRVLRVINYNKDHSGLYAGIDTGCADDEDDDD
DQGGTDKTCLLQEDSMDAKRMLISMRSVINGKSLDESSLAIKKDNFNFLAGTDKGFYLDN
SFFNSPVQGKFVAPRGTKIFKKCCDFLLNKGTGGVFARIFFTDWACIVSSSKGKNNKKAI
ESTLQIRNGGCFSERLTPSMFDNESEQGELFHDRYCPDFLSDYNKQNIFSEQAYKCSFLA
NPVCPAKNMLKRAKNIRLCITNAGTALISKIMAEVEKMGNARTFISNGTAIPFRLAENTA
CISVDNNRYFLIDGTYLLGGRLEGINLVTDMYTRCKLKAEKHVILNSLFSTEFISAALAS
SMEGTTMGRGLCLIEHVSYMKNTDSVSNMNKNFWSMAEDQEETDENEDDDDENEEDEDEN
EENTENTSVVKYEPVSKTAFSSSLKPPSIFIADEDYIFLSILYELAKATSDCETASSSSS
SSSSSSSSSKHSSSSSSSNKKRKQKDDVNSTTTALHALRKCYISCVDQKTGMPRMDVVYL
LRGLMNFGGMCTAIASGDGEKAHHMVQTLCSVALNIATKTAVVFVGTKGNNLKTTLVDLC
KRTWFERFTNINVTALNNAGDSSSSTQANLASFAGKKGIVIIDEVGHQGSFGSKKSSSED
DKDESASRSGNVDFGGSGGEMNSVDINEARNAYGDGGNSKIVFSNINRLMTESKLKVCDQ
EYDFISELKHEKNRKNACNDTKKRKRGGEIEDEGVECEEIERNDGKNDENGVRIKDPINI
SFFARKAHWWNCSSGVVSTTFKEKNIVYNMLHRGAMPFSIKDCTDSPWLNETDAVYRHCK
KPIEYEGKFSKSEVKTALKCILGKFGSKICDNESFESIIDENCQVNNLHSWNDCKEDIDE

FIGURE 3, Sheet 90 of 160

WNEKFMSKNKKNKQNMKIEDKVDAIMNIIQKNNGLLKWNTSFDRDGSPVLVCNPATERFS
EMITSSLSAQDMLEIKKYLGDNCLSTNGGVKKSVIDGNTSAPGVLIAYHCVYTGKISDDL
SKTNYPVLLPPPKKQHFVAVDDAAEKALLGPTLSNINIDSIRNIKTISRKLSSIIKDPEA
AKLLVDRDLDFMNMYERYDASLFDVVKKPSKYSFPGFTSDGSVVLSTSTSDCENVLSCLK
KRIEKDKMSAKNSGSFIRMCMDKNLLSDEKDDSSSNSSKNTSSLPKTDDNSSDIANFLSV
FGENRQQSSQFSFASNSSGGGDSNKEACFNVDTPKRRQLVSALQKHNSDGSSSIITEIAK
AIPQKNDVSSSITKHMLPGQFPSSLLKNMTSPQNSVMIRGIFQQGAKSSITVSPIMMSNS
YIFSFFVDEAMSKRLIVFPCDTTFVFENKNEDVKKIIGLLDRGMKYIHSSLMMERCIKFG
KHGIKQRQHEFNHHKKAWNDFSGHSSDNKKKDRISDVSSVLPSVLMKNLIRNKVLELRDV
KSVSRLEENTNTFFHLYTSMSLCAKAATNYGESSSSSATITEVEEDNSCDAEEQQLRRKK
PANYESMCNKLPSPLQMCQINPKSLNTMAMNIARSRQGAWAQLNSMLNSVLFVEMPFVKT
TRFFGRDFNIKMHSPATKNRPAINFDNCIGMSLPNPDMDVVGYDKEGELIGVGSSLTKHL
CDAWGSMDVRDLMYSCHHLHMLFEMALQYTECKRRLSSLKTLKSDKTGVDYVAVMLACMV
YQLMVSNLKYPVFLSSSSHKRANTEDIADENQVSSLSVPMFLAMVVNKPLHALRHSTNLA
LPNASQKSDHSDIVKYIVMNQWGLRLNPDYLCPNCVKHVL
(SEQ ID NO: 167)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
SR40_YEAST (P32583) SUPPRESSOR PROTEIN SRP40	54	2e-05
Q9Z1T1 (Q9Z1T1) AP-3 COMPLEX BETA3A SUBUNIT	54	2e-05
AAD56625 (AAD56625) NUCLEOLIN-RELATED PROTEIN NRP	52	7e-05
P90493 (P90493) HERPES SIMPLEX VIRUS TYPE 2 (STRAIN HG52),	52	9e-05
P70475 (P70475) NEURAL ZINC FINGER TRANSCRIPTION FACTOR 1 (	50	3e-04
O95815 (O95815) DENTIN PHOSPHORYN (FRAGMENT)	50	3e-04

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 1064 to 1 of CT520: this corresponds to nucleotides 196778 to 197841 of the genomic reference sequence.

TaqMan Primer/Probe Sets:
5'start=7375
5'stop=7397
3'start=7450
3'stop=7472
5'primer=GATGACGATCAAGGTGGTACAGA (residues 7375 to 7397 of SEQ ID NO:166)
Tm5=57.66
3'primer=CCATTAATGACAGACCGCATAGA (residues 7450 to 7472 of SEQ ID NO:166)
Tm3=57.78
probe1=CAATGGATGCTAAGAGGA (residues 7424 to 7441 of SEQ ID NO:166)
probe1start=7424
probe1Stop=7441
direction1=Reverse
Tm1=68.98
score1=1.98
length=98

CT601
Nucleotide
Genomic coordinates:
Start: 1511
Stop: 1196(SEQ ID NO: 168)

Amino Acid
MYLSHIRQTPLVEERRALTFKMYHHNNNNQHSFVNCQCRRTSSSINCSSCSRETFNSVKA
IQYFNKTSRNNTAHHFKMPASKDRNYSSFEYAETAVAAHNISQW
(SEQ ID NO: 169)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
YT66_CAEEL (Q11082) PROBABLE G PROTEIN-COUPLED RECEPTOR B05	32	1.4
O00885 (O00885) MAP KINASE KINASE PROTEIN DDMEK1	30	4.2
CHD1_HUMAN (O14646) CHROMODOMAIN-HELICASE-DNA-BINDING PROTE	30	4.2
O97292 (O97292) PFC0965W PROTEIN	30	4.2
O96226 (O96226) SER/THR PROTEIN KINASE	30	5.5
O96563 (O96563) C-13 ANTIGEN (FRAGMENT)	30	5.5

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 353 to 3 of CT601: this corresponds to nucleotides 1184 to 1534 of the genomic reference sequence.

TaqMan Primer/Probe Sets:
5'start=96
5'stop=116
3'start=142
3'stop=162
5'primer=CTTTGTGAATTGCCAGTGCAG (residues 96 to 116 of SEQ ID NO:168)
Tm5=58.03
3'primer=AGTTTCACGGGAACAGCTTGA (residues 142 to 162 of SEQ ID NO:168)
Tm3=58.43
probe1=TCTTCCTCCATCAACTGT (residues 124 to 141 of SEQ ID NO:168)
probe1start=124
probe1Stop=141
direction1=Reverse
Tm1=68.98
score1=1.98
length=67

CT521
Nucleotide
Genomic coordinates:
Start: 272387
Stop: 268691(SEQ ID NO: 170)

Amino Acid
MSKSSSSTVKSASFFNSLMENAPSSKIELLEDGWTKKAAAADTDTPTAKPTGLSISLMDI
SGSMGSVKSAVADSCSGIMATLNVIAPGIQNAIVYYNDFDKHSIESGPVVRAPDCSEWEG
GDFVKHMRKTEVCGGGGGGSEALHSSLMYVFNNMIPAFKKMHGITRDEKFPILIFVFTDE
DVRIANSDTGKLCANSYDSETAPEEEFIMKTWGQKPLTILDMRKALVENDCWLRILNFSR
CSGSNQSELCQEDVINFSGYDNNRWQLFESFDRRSCNVRKNIATFIMRQSISLFKNLNDQ
FSAFPILREINQEELNVFIESEGRSEPAGFEKYGDAQRESFKSRVLNMAPLDFGRVVQGG
GRYNNHKRSVFLNCAYDSAFCCSKQTFNPQQQQQQQQSSSGGGGISKLAVVTQRAQSITG
GGNAASTLALHMNACFQSLDDFGIDHTNLCDCKGCTKLMASVEATSDQGRKTKLSRKYAR
VHWAKMFAEKLFKMMIKEQSMMYACSAVPDEIGAIYAFVTGNNAGVCSRVSTILSDLGTE
CGNKAEYAFLKEGKHMKSASYDALQVINNTDLTPEQSSMFMWFYVPNDALEEAGKIFHQS
FSFSNSYTGGGLLSLDEYKRFEFGQCFDFIKKLVSCLKITRNVEDVLLETSKTSNRYFAI
PVFCGSDDQKEVLREELASDLFGGREDVAEMMFIDLETVIQKLGTLYDVRLSLPEGGYAA
IKSVCAAASWAASCEVPSNTSNMILSIAKMAFTKYYQEQNSSSETDLDIILPSILEGTAD
GEIENNLSGVVFLRCLITWANKIGVDKNFTNKLEHFLALRILTKAGDSKIGEKYETFPVR
RLDLSEKDLKYICKRCGVKSLKMEYDNDEKLCLRCKGNYRMGKPMVYHWDNKLTRDPRAK
TASPTTLNLLNAKKIDDKVKEMASDIIGALNLPPTDKDNEIAVSAAAKAVGILYGKTCLL
YKLLNEGNIDIPVAVCVECDCCKSKYMMSTLGPDKPQNRKCPWCRYANKLVAMGRGGKKL
LMDLIECGAPSLAMVEEAIRTSGDVMYEELGEGEEFYIIDYFLKLKNTAIAEGNKLQQNN
NKRPAPLQVTSPSSPPKKMRSDLPDSLLAAIGECAIETKEKTTVNLIGLGEVKVVENVGP
NDLDGKDPFISLQEYCSWDKFNSLFVNPWLGYRLDEQWDDWNTFLIHVKKNDVWKFLCNK
TSPFSVVVMNDGSGLLNVDNVNVLVRQKICV
(SEQ ID NO: 171)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
AAF04634 (AAF04634) HYPOTHETICAL 45.2 KD PROTEIN	76	1e-12
Q9Y1T1 (Q9Y1T1) DNA POLYMERASE ALPHA CATALYTIC SUBUNIT (EC	36	1.3
P91805 (P91805) ARYLPHORIN GENE-SPECIFIC BINDING PROTEIN-2	34	6.4
O45322 (O45322) DY3.5 PROTEIN	34	6.4

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 1 to 895 of CT521: this corresponds to nucleotides 268736 to 269630 of the genomic reference sequence.

CT602
Nucleotide
Genomic coordinates:
Start: 2996
Stop: 2702(SEQ ID NO: 172)

Amino Acid
MDILEDIYKSAITLVLQSPEFVNDVKQEASQVVEGLIPSIREAVFRRLLEEERKKHEDEV
GDVEDKRQAVIDKANTMITTMAAEYLESVDILEEFGF
(SEQ ID NO: 173)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
CRCM_HUMAN (P23508) COLORECTAL MUTANT CANCER PROTEIN (MCC P	36	0.055
ACVS_PENCH (P19787) DELTA-(L-ALPHA-AMINOADIPYL)-L-CYSTEINYL	33	0.48
ACVT_PENCH (P26046) DELTA-(L-ALPHA-AMINOADIPYL)-L-CYSTEINYL	33	0.48
Q9XJC5 (Q9XJC5) HYPOTHETICAL 26.4 KD PROTEIN	32	0.62
NOSZ_ACHCY (P94127) NITROUS-OXIDE REDUCTASE PRECURSOR (EC 1	32	0.82
EZRI_BOVIN (P31976) EZRIN (P81) (CYTOVILLIN) (VILLIN-2)	32	1.1

Comments:

TaqMan Primer/Probe Sets:
5'start=121
5'stop=144
3'start=200
3'stop=222
5'primer=AGAGAAGCTGTCTTTAGACGGCTT (residues 121 to 144 of SEQ ID NO:172)
Tm5=58.14
3'primer=TGCCTTGTCTATCACTGCTTGTC (residues 200 to 222 of SEQ ID NO:172)
Tm3=58.14
probe1=AACACGAAGACGAGGTGG (residues 164 to 181 of SEQ ID NO:172)
probe1start=164
probe1Stop=181
direction1=Forward
Tm1=69.14
score1=1.85
length=102

CT522
Nucleotide
Genomic coordinates:
Start: 276736
Stop: 275206(SEQ ID NO: 174)

Amino Acid
MASGFAIKGIVKNYRRIPSIIESIKSIRRSELAEGVYIVSLHKNTPKHEVDEIVNKIRLS
AGNPCLEKTSLFLQHHSQMRNFYTRKGAESESDWLKRLPEDLRNINNIVKREALPHDKSF
TFSPLYRILTDRLFNAAIHNCKYIIVTADLLMGCGITNNKVEKKLLSMGSILGGESMVPL
HDIAHRLSYKGLRIENPIVGSCHDQCLVVPVSMLGKIFSSNMYPTFKNFDQCMALFLNAV
VTHSAEKMDGKHERNKVIHMPNEVYLDAARRKYLEEKLEETNKLDAIDEEAREEYGNEIG
RIGDKSTCLVFALSARDFFLTNRFNEDTPLYSGTERGIRFMCSNYCTMRDEGGFRPRLIM
SAYGPTSYPIIFNTLYDQFNVQYYPCVSGVVLSFIGDDQLAPEPESLVDIVVRSIKNPSI
RIFSGDGETVYQDGRRVDVGGEGKNQKFNREERTILNVLRIIKAYNEERTKEDEDEEEEE
EEEEEQQTAATVTVESDWDLSLERGENWV
(SEQ ID NO: 175)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
O61310 (O61310) TSJ5	44	0.003
CINA_ELEEL (P02719) SODIUM CHANNEL PROTEIN (NA+ CHANNEL)	42	0.009
MYC_BRARE (P52160) MYC PROTEIN (C-MYC)	41	0.019
Q9Y0C6 (Q9Y0C6) J5 PROTEIN (FRAGMENT)	41	0.019
O35788 (O35788) CYCLIC NUCLEOTIDE-GATED CHANNEL BETA SUBUNI	41	0.025
MYC_CARAU (P49709) MYC PROTEIN (C-MYC)	40	0.033

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 374 to 1 of CT522: this corresponds to nucleotides 275340 to 275713 of the genomic reference sequence.

Hit to public SBV sequence:
gi|6007410|gb|AF178573.1: CT nucleotides 1 to 552 match nucleotides 555 to 6 of the public sequence with a 99% homology, a score of 1063 and an Evalue of 0.0

TaqMan Primer/Probe Sets:
5'start=682
5'stop=703
3'start=767
3'stop=787
5'primer=AATTTTGATCAATGCATGGCAT (residues 682 to 703 of SEQ ID NO:174)
Tm5=57.93
3'primer=CGTTTGGCATATGGATGACCT (residues 767 to 787 of SEQ ID NO:174)
Tm3=58.39
probe1=CAGTTGTTACACATTCGG (residues 716 to 733 of SEQ ID NO:174)
probe1start=716
probe1Stop=733
direction1=Forward
Tm1=68.99
score1=1.99
length=106

CT603
Nucleotide
Genomic coordinates:
Start: 24906
Stop: 24660 (SEQ ID NO: 176)

Amino Acid
MTCPEISKHISGTDRRFWNTADPGGLSYPFNPLFTLHLHLKNFSKIFSAHSSLGGGPLTR
PYVKFEGWTAGSTQRQITERS
(SEQ ID NO: 177)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
CAB49803 (CAB49803) HYPOTHETICAL 69.0 KD PROTEIN	31	1.8
O74312 (O74312) PUTATIVE TRANSMEMBRANE	29	5.2

Comments:
Hit to public SBV sequence:
gi|6165655|gb|AF099142.1: CT nucleotides 118 to 231 match nucleotides 5652 to 5539 of the public sequence with a 90% homology, a score of 139 and an Evalue of 5e-36

CT523
Nucleotide
Genomic coordinates:
Start: 281865
Stop: 281127(SEQ ID NO: 178)

Amino Acid
MVSTRSMEAKAAAAAKAKEVSPTTSKRKAEDLTEGTEEEEESVETHPPSKLPRVDEDEVY
IDENVDGDVQILASSIEVARMERERLAEAMVRDIKIEEEKAATEARKEIASRLIYKEMVY
LLPQLENMTNRLRPRSLLRHNEMTITDRTFSDLQIFNKVTFEFPILTDIAFLAREKSRVE
GSRFYNDMKIGPITAYKLNLMCNKFIESVVQKVKAEISPFVEVSVSSELEGSPFWDFKQR
IVKHT
(SEQ ID NO: 179)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
Q23915 (Q23915) PROTEIN KINASE	43	0.001
O77819 (O77819) CORNEAL EPITHELIAL RHO-ASSOCIATED-SER/THR K	43	0.002
Q13464 (Q13464) RHO-ASSOCIATED, COILED-COIL CONTAINING PROT	43	0.002
P70336 (P70336) RHO-ASSOCIATED COILED-COIL FORMING KINAGE 2	40	0.017
P70335 (P70335) RHO-ASSOCIATED COILED-COIL FORMING KINAGE 1	39	0.029
Q63644 (Q63644) RHO-ASSOCIATED KINASE BETA	39	0.029

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 1 to 712 of CT523: this corresponds to nucleotides 281143 to 281854 of the genomic reference sequence.

TaqMan Primer/Probe Sets:
5'start=404
5'stop=425
3'start=502
3'stop=522
5'primer=GATCACTTCTCAGGCACAACGA (residues 404 to 425 of SEQ ID NO:178)
Tm5=58.93
3'primer=ACGGGCAAGGAAAGCAATATC (residues 502 to 522 of SEQ ID NO:178)
Tm3=59.06
probe1=AATGACCATTACAGACCG (residues 426 to 443 of SEQ ID NO:178)
probe1start=426
probe1Stop=443
direction1=Reverse
Tm1=68.98
score1=1.98
length=119

CT604
Nucleotide
Genomic coordinates:
Start: 50300
Stop: 49079(SEQ ID NO: 180)

Amino Acid
MSHINSTSAATTSSNTLPICTTTAPMIAAARAAAIASRTSASAVTSINSNSTSSSAMFRV
PQGISVTAMPPVPALTSLTESTGTRMSSTPNVDVIPVPGPKNKSKSKKKDSKRKKNQNGN
RSSDEDEPSLVIDDGSGRQSKNKKYSWVTSLATTTAERNNDTLAPPRPFLPTPEEGNMSE
IDAGLSNPVTRQITGEVYSAALTSGVGDNGLYPSHFTVADTSYGDCETPIPGPAFVLDDG
TVSRGTSLLHREEAEFLNDGSKVIHTVKPRNSKYSNIQRAASCMAYAVDLLNNHNITSDQ
FDFMAMTAWAARQRCGEMAKFFEKRDKDIGEYRNKVVQYNRGIFTRTTEMNKRAKIILEQ
QQRREAAAAAAATGATAPIPTTSAAGVGATSSATTNSLEYQEIRYQ
(SEQ ID NO: 181)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
AMYH_YEAST (P08640) GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.	55	8e-07
AAC49609 (AAC49609) GLUCOAMYLASE	55	8e-07
O39781 (O39781) MEMBRANE GLYCOPROTEIN	53	4e-06
O39782 (O39782) MEMBRANE GLYCOPROTEIN	50	3e-05
Q9Y075 (Q9Y075) PROTEOPHOSPHOGLYCAN (FRAGMENT)	48	8e-05
Q14888 (Q14888) MUCIN (FRAGMENT)	48	8e-05

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 1 to 666 of CT604: this corresponds to nucleotides 49128 to 49792 of the genomic reference sequence.

TaqMan Primer/Probe Sets:
5'start=572
5'stop=592
3'start=640
3'stop=658
5'primer=GCCAAATCACCGGAGAAGTTT (residues 572 to 592 of SEQ ID NO:180)
Tm5=59.06
3'primer=CAGCAACCGTGAAGTGGGA (residues 640 to 658 of SEQ ID NO:180)
Tm3=59.24
probe1=CTCACTTCTGGAGTTGGA (residues 604 to 621 of SEQ ID NO:180)
probe1start=604
probe1Stop=621
direction1=Forward
Tm1=69.03
score1=1.96
length=87

CT524
Nucleotide
Genomic coordinates:
Start: 291298
Stop: 289681(SEQ ID NO: 182)

Amino Acid
MEDFKQLKVKNGICLSGENTENYERVLLTFKSVKSVRRSELKEGHFIVRLRDKEVLHIKN
GNERLRQLTGDPTLQIGLKYTSSLPKQGSFLEDEDPNYGKKWNESLPSPFQEMNKIVEEK
ALVNDKNFKFSPLYRIIHERLSNAAVKKCDYMIITTDFLVGCGFSPRNCTRTLKNMEQVL
VQHGGTSSRVSVYDICDRLTYNGLSIANPIVGSFSNMCLIVPMDKLGLLFYNSTHPSAKS
IGNYMSCLFNAAVVYTLEKSNQKLDNFEKEIRFAKNEVNLLVSERSVLEEKLKESKKLYA
ASEEQRISLRDVHKKSSIASSRYDGGACLVFAFSDRDFSLLCRTNGNGSFYSATEEGIRY
VSSDDYRKRDVDERRPRLVMSITGSDAPICIRDSIRNHFNNHFIASGKGNEISFIDPPNE
RLLMEMVREVTGSDIKIFMDNGKVYQDGVEIKVIDPSSKEGKDIIKKEETLPEEERKRLR
RERRMIFNTVKAIETYNEERGEEEEVATSSGGTKRKREEKEGDYVALLNKACKEIKVC
(SEQ ID NO: 183)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
Q57105 (Q57105) FESMID CLONE 31, COMPLETE SEQUENCE	39	0.10
O94986 (O94986) KIAA0912 PROTEIN (FRAGMENT)	39	0.10
O94944 (O94944) KIAA0866 PROTEIN	38	0.23
MYST_HUMAN (P35749) MYOSIN HEAVY CHAIN, SMOOTH MUSCLE ISOFO	38	0.23
YDH6_SCHPO (Q92351) HYPOTHETICAL 140.8 KD PROTEIN C6G9.06C	38	0.23
Q22705 (Q22705) T23G7.3 PROTEIN	38	0.23

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 1642 to 1 of CT524: this corresponds to nucleotides 289650 to 291291 of the genomic reference sequence.

TaqMan Primer/Probe Sets:
5'start=723
5'stop=746
3'start=828
3'stop=852
5'primer=TGGAAATTACATGTCATGCCTTTT (residues 723 to 746 of SEQ ID NO:182)
Tm5=58.47
3'primer=TTCGCTAACTAGAAGGTTGACTTCA (residues 828 to 852 of SEQ ID NO:182)
Tm3=57.59
probe1=TGCTGCAGTTGTATACAC (residues 750 to 767 of SEQ ID NO:182)
probe1start=750
probe1Stop=767
direction1=Forward
Tm1=68.96
score1=1.96
length=130

CT605
Nucleotide
Genomic coordinates:
Start: 51809
Stop: 50423(SEQ ID NO: 184)

Amino Acid
MDSSASVVFMRFAPPGEETALPPRRATPGSVAYDLFPSEEMDIEPMGLAKISTGYGIDKF
PDGCYGQIVSRSGMTWKNNTSVPTGTIDVDYRGELKVILRNHSAEKSVPIRKGTSIAQLI
FLRYCDVEEEQIVYINETTGERTIIDSSSKKDNKNQARSVRGTGGFGSTDNPNFTETTVS
RNQQEENKKEELEEGEIVEMEGFIDIPFLEGFENILAEQSNETGVTYPNTNQDVEEKDTK
NIDVVRELEAEFSSGIGSGSMDSSDSSDSSSSSSDSSDSSDSSDSESSDDSEGGDNKVRR
IRRHQYHRRQLSYSDDVNGGGRNSEKMEMDRVTHIKTEHIKREDEPRYEERERYIHPRRM
QVPKDYYCEQYEHYDAPAAAHHHRHHQHRHQHQRHFNQPRSNNSSDVTAYVNENSPTRPC
RDRNSRFSERPNNGGYNRINSRYTTFDPYRYGARRGRGGVY
(SEQ ID NO: 185)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
Q89662 (Q89662) COMPLETE GENOME	90	2e-17
Q86612 (Q86612) ORF2	89	8e-17
DUT_CHVP1 (O41033) DEOXYURIDINE 5'-TRIPHOSPHATE NUCLEOTIDOH	88	1e-16
DUT_YEAST (P33317) DEOXYURIDINE 5'-TRIPHOSPHATE NUCLEOTIDOH	87	2e-16
DUT_LYCES (P32518) DEOXYURIDINE 5'-TRIPHOSPHATE NUCLEOTIDOH	83	3e-15
DUT_HUMAN (P33316) DEOXYURIDINE 5'-TRIPHOSPHATE NUCLEOTIDOH	83	5e-15

Comments:

CT606
Nucleotide
Genomic coordinates:
Start: 65024
Stop: 64010(SEQ ID NO: 186)

Amino Acid
MSSSQGLNNNMCTTEILLPKCTSSSLSLEESVDYLEKDFEELGIPLVEGKEVLLEFAYKI
LNKRDTIRVIGDEQGDVCSVFFLRFGKKKTFNPQTKMWLVKLANAIALSMGVVPEPACTC
SRMMTTAKKIPVPESYKNVNRNIQKFEDVHYIDINFQSFVREQIGLSVLGKNDVQKKKKE
ETPFFAPFNKSKIGGECIEDLKYDSESVSIIRDVFNLLGEMPTEDVKTSRSCINPSHNDT
NPSMRLVFRPMYWRNSKLVMDKLSKEQDSALIEKYMGGEHQHCIIGGRNVLLYCITALCF
SSDCGFKKMLTNDEIKQLIWYLVLLFFHIICPIIQSK
(SEQ ID NO: 188)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
YNHE_ECOLI (P77522) HYPOTHETICAL 56.3 KD PROTEIN IN LPP-ARO	35	0.69
TTK_MOUSE (P35761) DUAL SPECIFICITY PROTEIN KINASE TTK (EC	34	1.2
Q56333 (Q56333) FLIL	34	1.2
CAB49508 (CAB49508) HYPOTHETICAL 32.8 KD PROTEIN	33	3.5
BAA85006 (BAA85006) ORF1P	32	6.0
BAA85071 (BAA85071) ORF1S	32	6.0

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 531 to 1 of CT606: this corresponds to nucleotides 64063 to 64593 of the genomic reference sequence.

TaqMan Proe Sets:
5'start=546
5'stop=567
3'start=655
3'stop=677
5'primer=CCCTTTCTTTGCACCCTTTAAT (residues 546 to 567 of SEQ ID NO:186)
Tm5=57.43
3'primer=ACATCCTCAGTAGGCATTTCACC (residues 655 to 677 of SEQ ID NO:186)
Tm3=58.14
probe1=GTATGATTCTGAGTCTGT (residues 606 to 623 of SEQ ID NO:186)
probe1start=606
probe1Stop=623
direction1=Reverse
Tm1=68.79
score1=1.79
length=132

CT607
Nucleotide
Genomic coordinates:
Start: 68659
Stop: 65032(SEQ ID NO: 188)

Amino Acid
MGVPEAKKVYENAYGAQNGRVIKEKTGYEDCYDDEDDEDYCSGEEDCTTSSLLKATSLAN
INSKNFLDFGRGKKSSSSSPTCDYTLDMVDLPTYNVSDLVMLGRQIATTMLKGQKNMGQM
ILFINTTNQQIIDVLHDGFNVIREEDTMHSRMQNKKHIYENFYCRDEKKVISEFFSRKYK
HEKIKARIERVPIIIPSSQEEVDWLTEPPIEDMMMAPPVSNHKMDDYEGLDYWINKHTDV
MKKRKFLTNSFLFRNVPTTSFNSSPTAVLKSRFKDAFFASQMEGVILYYAFRMIRVMKNL
LKSKNLKGRYTVLFTDGKAPAIKMMTRAKRQIRQERSKEKAKSRNENCLNRKTNDLLFYS
CERMMMRLPQGLMASALLDIMRIPVLKTTGSKCMYLSNASFTEAEDDIVRLTSCLLNLET
PGKHFSLLEKRKILEYDSYNMSGNRKESKRWEDLLNVLKQHTNDENQTLSMNLFSHDSDV
LVKWNLMVGHHKNVCRLTGTQFKDSETFLKIGHVKFFRCMNSNSSGENQANELGGFAAKR
RTKPNTIYNLAESPLMLSPESTLLIMLTKGSDYNSAIVSNCEYDTWVRKEVAVFENTYCT
CVGGWEIFLSEQEARKNNKDCDDSVGNISMGNLSKSNCRKCDKKLVLPFWTIKFFYLSQA
IDFVRDPLQLCFPPTHLIDLETDVSLKHALHRALAVNAAANVMSYLTMGSFNQRVFGTIT
TLSDISIHLSGANNNESKNTGSDVESDTEDLIPFSNNKRKSGNDPQKSTRKKSKVNATRK
SAPVTKKLSSSVFESIRGFFESHTEGGIINDRGILTKERIDVFGNNLDTNPEALGEENGG
GGGIVSSIPGLSTEQTSILKTEQNNSTSDFLDFFKKFNEMDDVEEEEEKMEEGEKEEEEA
DLETDDWLDEARKAFEYKDSDFLEAVTAATNEMTSSLAKNNIEEDEHSRCSVSSKLNNKQ
PVMDEEKWAEIVNEFDKCISLDNITYNDNSLLSRLSGVLMDANKREDGNNSNVVLYEPVQ
GIDDERFSGVPYSVKTMNLLVIVYMNMCGLEDNTIVYQQLMPIIHSEFCGKTEEDKICTD
RTNFMSAALEYTMLQYMPELKKTPRIKQIKRKNWERIPKVLDDFKDKVSTCTDNYNKLLA
TLNKEGKIPSENTKWLPSQGQFMPVLGVAISKPWSPLTLWSSFYLQHQQRQDVSLTNITP
PNSPRPEQ
(SEQ ID NO: 189)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
Q12532 (Q12532) HYPOTHETICAL 119.1 KD PROTEIN YPL009C	50	1e-04
Q9XZI5 (Q9XZI5) RANGAP	47	8e-04
Q13387 (Q13387) HYPOTHETICAL PROTEIN 384D8_2	46	0.001
Q9YTL7 (Q9YTL7) ORF 48	45	0.003
Q25662 (Q25662) REPEAT ORGANELLAR PROTEIN	45	0.003
O96266 (O96266) HYPOTHETICAL 283.6 KD PROTEIN	45	0.004

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 1 to 860 of CT607: this corresponds to nucleotides 65102 to 65960 of the genomic reference sequence.

TaqMan Primer/Probe Sets:
5'start=1428
5'stop=1448
3'start=1516
3'stop=1538
5'primer=CGATTCTGATGTGCTGGTGAA (residues 1428 to 1448 of SEQ ID NO:188)
Tm5=58.31
3'primer=TGGCCAATCTTTAAGAACGTTTC (residues 1516 to 1538 of SEQ ID NO:188)
Tm3=58.35
probe1=TGGAACCTGATGGTTGGA (residues 1450 to 1467 of SEQ ID NO:188)
probe1start=1450
probe1Stop=1467
direction1=Forward
Tm1=69.04
score1=1.95
length=111

CT608
Nucleotide
Genomic coordinates:
Start: 69118
Stop: 68704(SEQ ID NO: 190)

Amino Acid
MDGDSSSLQLLSESEFDYVVETLKEQGVWELALEVFNEVSNSIETVKEEEDYTVLRSRNY
FPTESITLYKQQQEEEESTPIKKRKLASGKSPRSLCRELRLLQIPSTTTFKAAPRSSSRR
GKNTRLRRVCKNYGAHQ
(SEQ ID NO: 191)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
VE2_HPV08 (P06422) REGULATORY PROTEIN E2	38	0.028
FLP_ZYGBI (P13784) RECOMBINASE FLP PROTEIN	34	0.41
Q9XZS0 (Q9XZS0) GUANYLYL CYCLASE (EC 4.6.1.2)	33	0.71
CINA_ELEEL (P02719) SODIUM CHANNEL PROTEIN (NA+ CHANNEL)	32	1.6
GLMS_HELPY (O26060) GLUCOSAMINE--FRUCTOSE-6-PHOSPHATE AMINO	32	1.6
Q9Z8C4 (Q9Z8C4) TRANSGLYCOLASE/TRANSPEPTIDASE	32	1.6

Comments:

TaqMan Primer/Probe Sets:
5'start=114
5'stop=138
3'start=235
3'stop=259
5'primer=GGTGTCCAATTCTATTGAGACTGTG (residues 114 to 138 of SEQ ID NO:190)
Tm5=57.77
3'primer=CGAGTTTCCTCTTCTTAATAGGGGT (residues 235 to 259 of SEQ ID NO:190)
Tm3=58.39
probe1=AACAACAACAGGAAGAGG (residues 209 to 226 of SEQ ID NO:190)
probe1start=209
probe1Stop=226
direction1=Forward
Tm1=68.86
score1=1.86
length=146

CT609
Nucleotide
Genomic coordinates:
Start: 78365
Stop: 77441(SEQ ID NO: 192)

Amino Acid
MWCSTHLSYSEFFTPLQSQKLFRNFFRALEFRGWTASSTECQVPRVDLWVGPMSDYTRNC
WFQKRTLTFVCFWNRRFWRLVDPEMRGYNLLFSLENFTLPLSQKLFKNFFRALQFRGWTA
SSTECQVPRVDRWVGPMSDYTRNVIAPETYINFCVFLEQAFLETGRPRNERVYPSVFTRE
FYSSSISKTFQKFFRALQFRGWTASSTECQVPRVDLWVGPMSDYTRNVIAPEIEEVSYGH
FWTRCFWTKILLDGNPLPLPPPFKKGPRVYNDCTTPHSNHHNHHHHHGRTSILQQTLSRK
WSSLL
(SEQ ID NO: 193)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
DYRK_RAT (Q63470) DUAL-SPECIFICITY TYROSINE-(Y)-PHOSPHORYLA	37	0.22
DYRK_MOUSE (Q61214) DUAL-SPECIFICITY TYROSINE-(Y)-PHOSPHORY	37	0.22
O61543 (O61543) BHLH-PAS TRANSCRIPTION FACTOR SPINELESS	37	0.22
DYRK_HUMAN (Q13627) DUAL-SPECIFICITY TYROSINE-(Y)-PHOSPHORY	37	0.22
HXA1_MOUSE (P09022) HOMEOBOX PROTEIN HOX-A1 (HOX-1.6) (HOME	36	0.29
O60275 (O60275) KIAA0522 PROTEIN (FRAGMENT)	36	0.50

Comments:

CT1010
Nucleotide
Genomic coordinates:
Start: 41348
Stop: 41795(SEQ ID NO: 194)

Amino Acid
MTHLVLLILSLSLSPVYHHLTPYLSPHLTYTPISPITSIFPHLIHSLQFQHPVLAEPTHN
QIWTPVFPFIPNRHHLCPQALAVYIRRRGQARSISSLQASRRATQQALSLLLPRRDLPIL
KLQEWPLQPPPHQVLTPCWTLSYLVLRN
(SEQ ID NO: 195)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
O62081 (O62081) C31A11.6 PROTEIN	36	0.20
Q05330 (Q05330) PUTATIVE ORF	32	2.2
Q60974 (Q60974) RETINOID X RECEPTOR INTERACTING PROTEIN 13	32	2.9
P79230 (P79230) KAPPA CASEIN (FRAGMENT)	32	2.9
Q9WAL8 (Q9WAL8) POLYPROTEIN	31	3.8
AAD12852 (AAD12852) Y8A9A.2 PROTEIN	31	6.6

Comments:

TaqMan Primer/Probe Sets:
5'start=209
5'stop=227
3'start=280
3'stop=300
5'primer=TCCCTAACCGGCACCATTT (residues 209 to 227 of SEQ ID NO:194)
Tm5=58.83
3'primer=GCTGGCTTGCAGAGAACTGAT (residues 280 to 300 of SEQ ID NO:194)
Tm3=58.29
probe1=TATATAAGGCGGCGCGGC (residues 250 to 267 of SEQ ID NO:194)
probe1start=250
probe1Stop=267
direction1=Forward
Tm1=69.00
score1=1.99
length=92

CT1011
Nucleotide
Genomic coordinates:
Start: 41758
Stop: 42097(SEQ ID NO: 196)

Amino Acid
MLDSKLLSSEELKELTSYVSTSSRRSDMKKHLLHLFEEHEKIFQFIQGKHKFSLYTLDFE
IFYVMLNILLVEVKNILSPIPLLFDRNLQPVRRLWMFHNGPASPERCSRSLG
(SEQ ID NO: 197)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
O44068 (O44068) DNA POLYMERASE ALPHA (FRAGMENT)	31	2.3
Q49563 (Q49563) DNA, TRANSPOSON-LIKE ELEMENT ENCODING 3 ORF	31	3.0
BAA74885 (BAA74885) KIAA0862 PROTEIN	31	3.9
O44055 (O44055) DNA POLYMERASE ALPHA (FRAGMENT)	31	3.9
O76063 (O76063) LEUCINE-RICH REPEAT PROTEIN SHOC-2	31	3.9
YD89_METJA (Q58784) HYPOTHETICAL PROTEIN MJ1389	31	3.9

Comments:

TaqMan Primer/Probe Sets:
5'start=107
5'stop=127
3'start=193
3'stop=217
5'primer=TCGAGGAGCACGAGAAGATCT (residues 107 to 127 of SEQ ID NO:196)
Tm5=57.83
3'primer=CTTCAACCAACAAAATATTCAGCAT (residues 193 to 217 of SEQ ID NO:196)
Tm3=57.46
probe1=ACAAGGTAAGCACAAGTT (residues 138 to 155 of SEQ ID NO:196)
probe1start=138
probe1Stop=155
direction1=Forward
Tm1=69.01
score1=1.88
length=111

CT1012
Nucleotide
Genomic coordinates:
Start: 42053
Stop: 45491(SEQ ID NO: 198)

Amino Acid
MAPPHLNAAADLLDKVMSGPLSPEGAQTSSPAACVGAKVVKALVSFCQKTRFTTNIVMRE
VKAMEFQGDDFNYSALCASMPQRPVTERQMFALMKSEDEEMGVSANFSPVSDDVINPSSL
PSGQEVDSSTSAQISGMFQNVWSLLEECGSGSNSNSSPVSRTVLVCTLFIIQVFKFLVTK
VSNVNVLNQLFGHVVFGSLDVAPSNNNSVPSTVVNNNNKPSTSNNSNNISNKRVGGSNNS
GGGRSKKVTATAKNPFNNVDGDNHGMFAGAPVDVNLDDFVFPQVETLTSKSTIPKEEVNV
DEDLSKMCRKTALTPLEIHTFNVFISEINPSKYDRSMFCKGFLTAWDKFVEGDTAGVKRF
RNYILTRSNYASAARAVYEASIKGTVYYNDKSKFLFHDNVNPDLDKSWGNKNGKKPRLPA
NLMAFMGIDIVKVCAKGIQKYMFAKQFQHPEVEELVPPMAVYAKVAAGLKSGTLFDDWDL
PEYENCQFIKYDTEGCKKHSELYAKQLLRTGLNQYNKLEEGQSAFPFANIVTVTSASSDD
IHGDTIIELMYKTKDGVKGVSKIEDENIIKVNPAEEKKNNRVQAEKTLYFEIDSDDEVCE
RTEEEFFRPTSVVAAPTTPLVPSNVEEEEEEEEQMEEEEEEEVEREEGSDKEDDGDAPAQ
EEMEEEKEEEQQQQPEEESNGNENQEEEQQQQQQPEREEENKDADSDSDSDSSSSSSSSS
SSSSSSSSSSSSSSSSSENEAEKKKEEEVPAKIQKRKRLSERPSEAASSPKRMRVEEEQQ
QQLSPSLDILQTAVDEMMEEIPAPEPIVATTSPKAATLALKTGFSYSSFVRGDDLSVAGN
TSPTEPAAVPAAATCTSDVGNDFLDMLDGLPGDIVMQPGECDVTAKFFEGITLPDGTDNE
CTGFDDLLKATETDNIITTTCFTSPIHPSSNSAPRKDIDNCSSIKRSRAGSLFDTDDDSE
TNEVEKEAPKRKKHLKKRRNKSHRGSSGSASSSHCMSSDEESEDERDMKSTSKVHKSPKA
HVKHSPKYDAVNSDVNNSYNNVNSTTCMSSSDSDAEAQPKSHNKSHSRKHSSSSTSDKKQ
NQQCSINTQNVKKTVVQSPPSFRSFSPKKDELGDFLSRKHTKPVRPYNKKRDNVNTTNNV
VQRSA
(SEQ ID NO: 199)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
Q9YTL7 (Q9YTL7) ORF 48	101	4e-20
O95815 (O95815) DENTIN PHOSPHORYN (FRAGMENT)	99	1e-19
GAR2_SCHPO (P41891) GAR2 PROTEIN	97	6e-19
AAD46501 (AAD46501) LATENT NUCLEAR ANTIGEN	94	6e-18
O40947 (O40947) ORF 73	92	1e-17
GARP_PLAFF (P13816) GLUTAMIC ACID-RICH PROTEIN PRECURSOR	91	3e-17

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 1 to 955 of CT1012: this corresponds to nucleotides 44515 to 45469 of the genomic reference sequence.

TaqMan Primer/Probe Sets:
5'start=1345
5'stop=1366
3'start=1389
3'stop=1407
5'primer=CATCCGGAAGTGGAAGAACTTG (residues 1345 to 1366 of SEQ ID NO:200)
Tm5=59.57
3'primer=CAATCCTGCGGCAACCTTT (residues 1389 to 1407 of SEQ ID NO:200)
Tm3=59.65
probe1=TGCCTCCTATGGCTGTAT (residues 1367 to 1384 of SEQ ID NO:200)
probe1start=1367
probe1Stop=1384
direction1=Reverse
Tm1=68.99
score1=1.99
length=63

CT1013
Nucleotide
Genomic coordinates:
Start: 45950
Stop: 47825 (SEQ ID NO: 200)

Amino Acid
MSSTTSPSSLWDDDDDDDEEDEKDVKQEVSNRPPIFSYMETVSFSDNDEDDNKGEEECFG
SNFDMFGDSDNMPSTSTAPFPPPSTTTPLPTPRSIMDTDSDECDEEGAAAASAPSIAASS
SIPVGISEAELKKMEKKKRKEIKKLKKMMKDPLPHLYVGGEPPVAADYKTRANISLYKVD
PSIDMCGVAPPQFCAELPTPSIDVYTSSYVFPPPTPAMHNKKGSKKCQFLKGRKALRKWI
HENVCMAPPGKRGGVFLAHLEQRFLAEHGDEYKVPRMFVSRVLNKAFPNLIARADTLCSD
MTFYTNLCWIVNGVVVCFDKDDGGIHGDASEYATGENFDTVVFHKREEQKTNGSASKKRR
LTPDTSNMGTSTDVQEFQTMGTNTDMQEFQSMGTNTNPIETSSVGVNTNPLPNPPPRLVI
TPLTNDVPELDMMWLYSPSRGGGNSRMSANTGTSPLSNTPIPTCFTGGANVVVPNGFVPP
TFPLECDEDDPSIPNSYNYEEDKVFHPFYEYMAKYLSPLVPSYNKGQTCNVVQEWFKGSF
SLAKRRGTVPKFCSNISHAFFCNMDVCTAMCKWAKTVIRHGQYCNRCIVRRSCTSMLAYH
YIVCRDASCDVPKCRERVRNDMDD
(SEQ ID NO: 201)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
AAC97971 (AAC97971) FAS-BINDING PROTEIN	47	4e-04
Q19871 (Q19871) F28D1.6 PROTEIN	44	0.004
NUCL_MESAU (P08199) NUCLEOLIN (PROTEIN C23)	43	0.006
AAD56625 (AAD56625) NUCLEOLIN-RELATED PROTEIN NRP	43	0.008
VP41_YEAST (P38959) VACUOLAR ASSEMBLY PROTEIN VPS41 (VACUOL	43	0.008
O35613 (O35613) FAS DEATH DOMAIN-ASSOCIATED PROTEIN (DAXX)	43	0.008

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 1 to 934 of CT1013: this corresponds to nucleotides 46867 to 47800 of the genomic reference sequence.

CT1016
Nucleotide
Genomic coordinates:
Start: 52093
Stop: 54913 (SEQ ID NO: 202)

Amino Acid
MSEPSVYAFIDIKEIENGWEKEFGLLVQPGQKLAPFRDISYDSSKLDCDAFSCIPSDILH
SDNEKRVGECNFAEHTSVSFPVKNPEGKTLRHFTACGPGCYRRYKQRDPHTGLPVARGVL
MQDHVDHETGNKMCEYLNQSLVMWAAVPWIRPGDLTEGYNTTHVPGFAFKEDDERDSKRV
KYENVVISKAYCDFFKQYYDADSGSCYRSGWMKFVHLMFGQYFTNLSYNLANPKPYNLTG
NTWSDVVSVLTDNPIVDAGAAPSRSEMDEIITKKKFNVFPSEQTSARQKAENIIRSQYGD
GVEIDPSSVDALMQFVNREGVVGTEKKSDRLMRVADAVMDAAMRLQVMGLDDSQSRRLLL
KNMIKMSRNNPEYARHFSSSLKLIGVTLAIKRSVFSKGASAKRKETAINNGEQHRRSRWS
PETVTEEDALLFARENITEDPKHPAPFVDILHSPDINSSIKSGSSSSIWNDILSRISSTR
KLEEKASVFVKNLVVKVVRQFLDILEGKLFSDGYEWDDNIPLMIGVDQILREVIKAASNM
CARFASSALESSLVTGFIDSASAITSRLAVQLAARTFSVFLEESVIEFVVAASLRLAIQA
FADLATLAASALTVIGIVIFVIQVLGLILDLALGLGWYDHIFSPEDLKKQVLVFRREFAK
AGNVDVGVAQPVTPEEIVAINVFLQTEENGEEKKEEGARKSKIDFLQKYFHSTPLMGKKS
KFVYIQEAAQEYLGGRTMNAFGQRIITAADDSDTTTTTQEGRRDDETVTKKMRSIILETG
QTLKDYSSAVNYNASRLDYVGEEWVRNTALKEETRSNTTSDNLFKKTVSLASMAGAFLVL
GIGVLVASHITLLRFTNIGLAFAFAGLLAFIALMSISYINMNAMGVVNSDAIYRSTALVG
DIKTDPRRVGMVQRHVGVGAKYNMITDFVSPMLDEIESD
(SEQ ID NO: 203)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
O67140 (O67140) L-SERYL-TRNA(SER) SELENIUM TRANSFERASE	41	0.048
YD86_SCHPO (Q10411) HYPOTHETICAL 222.8 KD PROTEIN C1F3.06C	38	0.32
Q88606 (Q88606) (CRUCIFER) GENOMIC RNA FOR RNA-DEPENDENT RN	35	2.1
PME3_PHAVU (Q43111) PECTINESTERASE 3 PRECURSOR (EC 3.1.1.11	34	3.6
O81424 (O81424) T2H3.2 PROTEIN	34	4.7
O04260 (O04260) HYPOTHETICAL 49.5 KD PROTEIN	34	4.7

Comments:

CT1017
Nucleotide
Genomic coordinates:
Start: 55054
Stop: 58189(SEQ ID NO: 204)

Amino Acid
MDSLTNTVTLLVNDRLGNHRTNKPITEQDVENTLNLNSLERASLLKLYSVFIKEMQSYSG
CIPKNKYTNVQEIFEDGLITFEWRDGTKVHRSVSPSSPIPLSTKKSPRSSPSPPPSMPSI
KEEEFEEEFEDDEEIYETDENVEDFINGDGEDSEEEEEEDIIVDDEEEENEEGENKYVLA
FSNHLRRQTAAAAAAAAAAAAAADIEKKDKNHAVSAHDYTLSALQQQQQKLLQQQQQQQHQ
QRSSSEKVTSTPNKFNKFLLPSNGFSEQTELFVCFDVDKIAQYNGLVELDILPIVAEYII
NGLGLKCSMETPPVKPCRRKEVKDVWCQPKTSFENDAVEDKHLAFAESPILQRPRDFPIP
KKITAYFCLDDSVDIKNPWGSCPLLKSGSNFRVSEYSRHFNEFSGVKNDDDTSSNTCFIY
SQKNPNIEIVSKLNIEFEVMMEGIITHRKDLFETGILSDSSLATAMAFCHPKARVRNVAL
FYFSVYLPFSKITRKETIKCSETDKVHIGSDAIFSPPSDNPNISAHQNNNNNNNNNTSVN
IEDRPIRNNNISRKMTITNYQCMACKERCTNNCTNGNYPDRGNQHLSHSVKGEDFFKILN
NSKVDSLKKLSRVLIPAPPSGNYTSKFCDRSSMCHSFFCRGIEPVSTSFSSDSFEKTKLV
LYGKVVDVINSYSAIKTSHNNRIRVFFNSEEKDNKTIPSRAESAKNAFKDILVHECNKER
AVSYFEQNKLSSKDGHLSNKWWIELNDLNIMFEKHVEDFYKKCSKVNDAESLKDIFNDFE
KTCDKYKTAKRAIIGAQDPSTSTPSKKENGITRIISTLSEFHSKDEATVSALLDKTMLLG
SRTIMSGVRCVIRNNSVFSGFENKNTNNNWELEIRHYVISMGGAAVTKISDEDLEQFTPV
RGAVSVTTAPNDKLPVGAHQTWKDEQTLKTNTKRNSLYDSYNSKRNNRDNNKIKNRSLKL
SDFNWRTPNISIQEFNANKDDVNKKRYAEVVASAAPKSPSPTSSSSSNSNSSSPPLSPLS
PTVKNSNNKPLYIPPHKRMTTTAV
(SEQ ID NO: 205)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
O77033 (O77033) TRFA	60	7e-08
Q94463 (Q94463) K7 KINESIN-LIKE PROTEIN	59	2e-07
NUCL_CHICK (P15771) NUCLEOLIN (PROTEIN C23)	57	5e-07
AAD46501 (AAD46501) LATENT NUCLEAR ANTIGEN	57	8e-07
O40947 (O40947) ORF 73	56	1e-06
Q98148 (Q98148) ORF73 HOMOLOG	55	2e-06

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 1 to 215 of CT1017: this corresponds to nucleotides 57667 to 57881 of the genomic reference sequence.

TaqMan Primer/Probe Sets:
5'start=1741
5'stop=1762
3'start=1847
3'stop=1864
5'primer=CGTGGTAACCAGCACTTGTCAC (residues 1741 to 1762 of SEQ ID NO:204)
Tm5=59.16
3'primer=TTCCAGAGGGAGGAGCGG (residues 1847 to 1864 of SEQ ID NO:204)
Tm3=59.84
probe1=TGAGCAGAGTACTGATTC (residues 1829 to 1846 of SEQ ID NO:204)
probe1start=1829
probe1Stop=1846
direction1=Forward
Tm1=69.01
score1=1.98
length=124

CT1018
Nucleotide
Genomic coordinates:
Start: 58947
Stop: 60029 (SEQ ID NO: 206)

Amino Acid
MKICQISSPTLTLSIPLEGVYHVKQLLHLKVHLDVKGVKQLLHLKVRLDVRGAKQNPWRK
NLCLLKKNVKSAKQLPHLKVHLDVKSAKQLPHLKVHLDVRGAKQLPHLKVRLDVKSAKQL
PHLKVHLDVRGAKQLPHLKVRLDVRGAKQNPWRKNLCLLKKNVKSAKQLPHLKVHLDVKG
VKQLLHLKVRLDVRGAKQLPHLKVHLDVRGAKQNPWRKNLCLLKKNVKSAKQLPHLKVLL
DVRGAKQLPHLKVLLDVRGAKQLPHLKVLLDVRGAKQNPWRKNLCLLKKNVKSAKQLPHL
KVLLDVRGAKQLPHLKVHLDVRGAKQQQQLCLPLKTISTSFTHLLLCLYMEYGKHQNLQV
X
(SEQ ID NO: 207)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
O41125 (O41125) A643R PROTEIN	36	0.34
O77336 (O77336) PFC0425W PROTEIN	35	0.75
Q65683 (Q65683) 42K TRANSPORT PROTEIN	32	6.5
Q48275 (Q48275) HYPOTHETICAL PROTEIN (FRAGMENT)	32	6.5
Q89659 (Q89659) 42K TRANSPORT PROTEIN	32	6.5

Comments:

CT1019
Nucleotide
Genomic coordinates:
Start: 62203
Stop: 63019 (SEQ ID NO: 208)

Amino Acid
MDVEFGFFHGLLSKALLPDEKHQPVIRRLCADDSRNKGEDGCCSFCGRRGTGESNTACLE
QLIDVCSFIGTVSSIGTIINSNLSTSCSRLQKTSDSYAALSHSSFLDVVYPSLKKTTEDV
LPHSLRAIWNKQLPKLYEKTLQPIEEEDIGYKDYVVSIEDDDNVDDGDQQEQMIIDEESY
KTIGEKSTIELIGMYNNNKFGNEFIRIPLRETALHAQSLRYDTEAKFVNHKDSIPLFYEN
STCTCKERLIDFSERQLQQLKQDGMDKPTDK
(SEQ ID NO: 209)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
AAF02799 (AAF02799) F5I10.23 PROTEIN	37	0.14
O23058 (O23058) BAC IG005I10	37	0.14
OPI1_YEAST (P21957) NEGATIVE REGULATOR OF PHOSPHOLIPID BIOS	34	0.90
Q24042 (Q24042) HYPOTHETICAL 89.2 KD PROTEIN	34	1.2
Q24043 (Q24043) HYPOTHETICAL PROTEIN (FRAGMENT)	34	1.2
O76871 (O76871) EG:100G7.2 PROTEIN	34	1.2

Comments:

TaqMan Primer/Probe Sets:
5'start=292
5'stop=313
3'start=375
3'stop=396
5'primer=GCGGCATTATCCCATTCTAGTT (residues 292 to 313 of SEQ ID NO:208)
Tm5=58.17
3'primer=TTGTTTATTCCAAATGGCACGT (residues 375 to 396 of SEQ ID NO:208)
Tm3=58.03
probe1=CTGAAGACGTATTGCCTC (residues 350 to 367 of SEQ ID NO:208)
probe1start=350
probe1Stop=367
direction1=Forward
Tm1=68.97
score1=1.97
length=105

CT10000
Nucleotide
Genomic coordinates:
Start: 3143
Stop: 6956 (SEQ ID NO: 210)

Amino Acid
MVLTLSCTTRRVASSKGNFSKEDAVLGNQFPILKKSNNLSIARPPSIESFSASVEKIFRE
WNESGGEKIFDISQNEEEWMDIISLVESVYEPVFSKSLKPDKLADKTCLTAAAFAALASA
VDEKLTILSGSDGSVLQRTTKVMKKDPKKIAESLLNNEKWTSILLDRLKTAKKLLSRRGA
LKSAERVEVLHRLNKLKEAPLPHHPSLFDNFSGGKTSAVSAGTVIASDMHFKLVEHIFKV
SFRKWGPCGDKTESGEEEDEEEEEEEKKHSISRFVLQFMNGHNGQHYHRPESASVYFCDY
YDYLAYRNLPNEYKLSSMHPGTFNMEDLPFRPFAVPSTYKTELEYKRFVQSTNLPQLSFD
YGEFLCYCIFGADWYKHLGDVVDSLENSSMISFDSQTLSGVYKNTANYKRLGKKRNGIAD
LAVRSMAEFIRTEAHKALTAEEMEEEEEEEEAEEEAMDQEPAEVDFLSVPHLRRKIRQAV
SVLNNFVENDLSILVSNFKNVLTDDTVSGTDTDNFGSSGEFEALSSHLFLSRILDEVHIL
RNTDIQRTLFSTHVSLSDKSPPSRVRGSNVNFNNNAGNISSLQTYGGIEELPENVLVGLS
GGFEDTDMYSGEDVVVVWDGCDGGKVLSVTFNCGDNFIQLHEKTAETFKDDTDLVERIRD
VLQTASKTGNLNKKAYSRKNIYAVLRENGIERPGDDFTEKGIALKDKTNQPPPPARSAKI
TVEGVKGFFSGFRDILETRALTTYSAETFRDLGQGIVKETEGLTAATVAETSFSEGLAES
LRSDANLGLEFSEDAKTVVFKNDTSRSLLEETRALRANNTSFSSFARDMGVQVSADLDAE
FAAEMRETYPDAALEQNLKDLDKFEETIPESQVKKLKKIDSYLTENPERAGKEINDTELS
KATDSVLGKKLGNAVTVLMNNFGKVTIVVGASVVAGFLGPAAVALVHASRGAHLNVVDHT
SPKGVISYKIVDFSCADRNTGWAKPTKHPFREEIDHVIALDASFLTENGAYVFPEDGGPK
SKYKAYAPICGTKDAAQGECGSWATFDDPHSVLPWVASMKDLPKGQSLSCDKGMSTLKAV
SSVLLSIGKDVAEAIFEVAEDAVVGLASKAISAVINNPLFIFGVPLGFGIAATRLNPSNW
KTGLIVFSILLVVILIVRFFAGSGPLTLNWFGAKNSAKRKQTEQFEDGGGNRSKIVLAEK
DNANSKLQSRRNETGPMRLEELPGHEDLRPVFFPATTNYSKSAKILGYKSKPFNDFYTKI
INTDIIKMDR
(SEQ ID NO: 211)

Top Blast Hits Sequences producing significant alignments:	Score (bits)	E Value
YKO6_YEAST (P36062) HYPOTHETICAL 75.5 KD PROTEIN IN SDH1-CI	43	0.010
Q12532 (Q12532) HYPOTHETICAL 119.1 KD PROTEIN YPL009C	43	0.017
O75184 (O75184) KIAA0702 PROTEIN	41	0.050
O60721 (O60721) RETINAL ROD NA-CA+K EXCHANGER SPLICE VARIAN	41	0.050
O43485 (O43485) RETINAL ROD NA+/CA+, K+ EXCHANGER	41	0.050
AAD28522 (AAD28522) FLAGELLIN (FRAGMENT)	41	0.050

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 1 to 969 of CT10000: this corresponds to nucleotides 5867 to 6835 of the genomic reference sequence.

TaqMan Primer/Probe Sets:
5'start=2102
5'stop=2125
3'start=2185
3'stop=2204
5'primer=GGATTGCTCTCAAGGATAAAACAA (residues 2102 to 2115 of SEQ ID NO:210)
Tm5=57.56
3'primer=ATGTCACGAAAACCGCTGAA (residues 2185 to 2204 of SEQ ID NO:210)
Tm3=57.81
probe1=AAGTGCCAAGATAACGGT (residues 2148 to 2165 of SEQ ID NO:210)
probe1start=2148
probe1Stop=2165
direction1=Forward
Tm1=68.99
score1=1.99
length=103

CT10001
Nucleotide
Genomic coordinates:
Start: 17098
Stop: 20842 (SEQ ID NO: 212)

Amino Acid
MGAPTNADFTRTVSGVASSLYLVNPGAPSDREKLVLASSYSDSFVYNYKDAVVTAEAPKW
CPFNEPALHEHIMNRLEKAGLINRSRFVCNPVKSAGEVCGFRYSGGSTPQNLIFPIGASE
INWLVILRNAARFGTVAASAKDAIERIPDLREGGTSKHVAKNAMRRLRVWRAFNWIAEAS
RSAGMIRYEPFSVGCALYDHEVRRRQLKGSYERNVLFLGDHFCKESTLLADISRGGRSSD
FWTIVEAVIRYKNRHARTISNETNAIPEDSSINLEWEDVLVKNQRDTNQGDDSTLEKTLE
AAIKEHESIGEKRKKHILEFIKTCLTEEQREMIFKGVGGKGNLSPAHLTNLADAILANNA
KAGIWVIMQSLLKQINFSILHLIGYEAQRLLMFKLYMPALLALFISQRGIGDVFLNGVFN
LEVMKERAANAKIRDMVSRDAYKNNTNESNNLGNYSQFDIATIYGQMSDCNAIPLSINIG
VPLHKSRMNMQDIEKTIQHIVDMGLAKIRVAEENRVARRLLHRRKMQEKAARERAAARQR
RLRGEEEEEEEEEEEEEGEEMEEEEEEAGTSGVNGSGYDQEEEDDGEEEEEEEEEEDEEDS
EGEDMNGENNSRKRKNTGNTSSTQQPPQKRQRGKNAPISTKGKRLKERDNIGGFLLATIQ
NDDRQVNVESIQKLLTARQRKYVKGGKCGDNGLPELLIEKVTNLLDSVFHFRKGSILNSI
HANRRSETGVYTTKANCICDYYERNVSKDSSNNTPHSSECIERARERDASCAESNKRPCP
VDSNNPEDVEQRMRELIMDPPSLSGVEDSLAIERVLQNEILFTSLVTNPIFNAVLGAEKG
DLGRFIVLNNIVKFMNMTIACLVDGDMPMLLDSRGKTKNLLEKGTVKNTRKFFKPNMTAA
ELNVATAQSAGHQYMNAGHCPEPGIKQMLLPDCIMKLKSIAMEKGRGGRSALHRQKCDHA
FCKMLKCLFFNIDPSNAADTFIDPASRATLFRLDDLCRDRKKYKNIDWVKDLLDPVMKGT
NKWVGTGEYTNIGRDSNVAAPVDFYTILKYTMIDDGVISVPSRKPNDVYYSTIERADDLL
TESRDASCESYRPTLFDARAVLEVNGDGRVPYPSSETVEDLGGEEEEEEEITGVIDDSTEI
EDVQVQDSNLFDVELFDIPEIEQHQQGGEEEELPSAISEVFASLPADNDSSSPAHIPSFG
NSEEGEKSPEPYNIFDSALDQLLDLIDSDGRNNNPKRVDWNSVTIQE
(SEQ ID NO: 213)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
GARP_PLAFF (P13816) GLUTAMIC ACID-RICH PROTEIN PRECURSOR	77	6e-13
O94922 (O94922) KIAA0835 PROTEIN	76	2e-12
Q9YTL7 (Q9YTL7) ORF 48	75	3e-12
CENB_CRIGR (P48988) MAJOR CENTROMERE AUTOANTIGEN B (CENTROM	75	4e-12
Q07034 (Q07034) RNA BINDING PROTEIN	73	2e-11
NAB3_YEAST (P38996) NUCLEAR POLYADENYLATED RNA-BINDING PROT	73	2e-11

Comments:

CT10002
Nucleotide
Genomic coordinates:
Start: 20783
Stop: 23729(SEQ ID NO: 214)

Amino Acid
MEETITLKESTGTVSPFKNENITRIASNYVRAFTDTWSHLVNISGAPLTAEKNPSAIPAN
ELNRYWTKTNVLCNPLFKLEDHITRDEDTGTITLKFKMYIDDKNGLYQSAVLMLALDSFV
SLASFSHGADLVSNKSENKFCVKIPHDTRAESLLNNVGFPAGLSGPFKRWSINYKAANLS
GKSGIDGLSGSMLTVLKNNTNKRATDILHLVNNVSASAQQLDDSEMSRTFNHQKKVGVCY
DINVSSSRQVNQRNLLHHQNIIGQHLIEFRTKQLERAQNKKVKEEENGEHEEMTSEEEEE
EDEYEEGGCLSDIDEEDFYEDGYDEEEGDDNRTRKKKKMEEDEEDEEEEYDDEEDEEEAE
TCGANGVIDCEDDAIIFPNGQNSKRKKNGKKTNIKKRSRRKGECSANTLSFVEKYVGNCK
SLGIKPVGCPPPSTEFTSLFMKGSEADSCYNTCQSTRGASRIRSLLNKYSVKDLMQVNSP
SSWKWANPPDRRFVLFDKKTKEEVEVKFEIECEKSEYFDVVSELPSNIKVWLKETAKIIK
HLALIEDFLPAMGAATPKIPLNLIKTMTSIFSVRDIVGFKIPEEVLSFIPIEWKTSISAM
GLLSVQFDRIIEVIDLMITNGAFATSCLNNAFFLERGVVPRDGSNTWLHTDLVQLSTSIF
RSIRNRGVNIGGNNNTGSNSSSSSCGGNKGDYGVRCGLSISKRGITLKPPPAAMTNSSSP
SSSAMISLPQPTRQSIDLSITTIIQDFSEVSGKLRLNGLQKNMSDKSKDVFNDAIYDSGA
FKALLTCTVNDKSRRKRKRRTLLASGEGVVRRNLMVSQGNDVNDAHQFQEECGIKIGGGA
SRVYKRAQRRGSAVSSRRRVRNKPQFTIAVSDEDDDCEEEGDFSSELNPTHSQLLLFQQR
QQDSCTEDDDVLVSVEEYNNRVSGSSTTAGDRVLAKDLLSTVSPNEKRNSAALAALTISR
HSLFNALSAKTKLGENGRFFL
(SEQ ID NO: 215)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
Q9YTL7 (Q9YTL7) ORF 48	75	2e-12
GARP_PLAFF (P13816) GLUTAMIC ACID-RICH PROTEIN PRECURSOR	75	3e-12
Q07034 (Q07034) RNA BINDING PROTEIN	74	4e-12
NAB3_YEAST (P38996) NUCLEAR POLYADENYLATED RNA-BINDING PROT	74	4e-12
Q9YPA9 (Q9YPA9) HYPOTHETICAL 45.2 KD PROTEIN	72	2e-11
O40947 (O40947) ORF 73	69	1e-10

Comments:

TaqMan Primer/Probe Sets:
5'start=1699
5'stop=1723
3'start=1773
3'stop=1797
5'primer=ATGACGAGCATTTTCTCTGTTAGAG (residues 1699 to 1723 of SEQ ID NO:214)
Tm5=57.07
3'primer=TGCAGAAATAGATGTCTTCCATTCT (residues 1773 to 1797 of SEQ ID NO:214)
Tm3=57.23
probe1=ACCAGAAGAAGTGCTCAG (residues 1743 to 1760 of SEQ ID NO:214)
probe1start=1743
probe1Stop=1760
direction1=Reverse
Tm1=68.95
score1=1.95
length=99

CT610
Nucleotide
Genomic coordinates:
Start: 85707
Stop: 83427(SEQ ID NO: 216)

Amino Acid
MPPKHKPNTALKKHIIRNQQRKKEDDAESRFQRNMGQEVSKLDAPTSSKNRQRRKIRTSK
ILSRSGDCVAGDCSDLENDEGKRDTDQEGGGRGGGNEEEEEGKEEGEGEEQQREEKEEQS
EEKEEKDGEEEEEEENVEDEHVTPTTSVSKRAKQMKKHIFPPSKKRKRSDTESKALAVPAG
KMMTVSRPLRGAITSGSILGVRSENAPQYDYVSYLADEAVVKEKAIQYRIRSLLANLLKA
NKTKAFPTSSSLLSSEQGKKKFGGKRTNTFVVTNVGAELVKALLANSCWAISHRKDIRSG
EIQWQELSSKILKSLNDGNATEINNLMSSIVEDRIQRTVKERVYFEQLATVCNNLFGTRI
LPNKNFDKNFVSVASDNSNATVRGLSIPRYFRAINNNVWVKMSSTMDLLVGGGMRSKSEH
SISMLEKCAAGVLARASARPVEKMIKSAVEETSQAFNLSTGVFVPKQQQQQRQQQQQQFP
PFQPPPFPLPPPQAPFQVQQPTYQGYLNPYYQYNQYYNPYAPQQLQQQYPLYFLGNQSQP
PPQLQQQQQQQQPPQPPNNIPPPPTPQQQSPSNIPPPQQQQQQPFPVQLISSPPPPPPIP
NTAPSPPISRVRFDSRSTTPQPPPTPVLPKPTPLPPPSTARAEEENATDMSFTDIDSELG
SIDFDLPPATPGRNVEEIIKAQRQAVKETGVRGEEEEEEEAFIAPIIRQPRTPGNFRDEL
LDVNESIYGSDIEPAAAAAAFDWDMGLDDLNGDEPYEFE
(SEQ ID NO: 217)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
P93794 (P93794) LOW-MOLECULAR-WEIGHT GLUTENIN STORAGE PROTE	84	3e-15
Q05573 (Q05573) OMEGA SECALIN PRECURSOR	83	5e-15
AAD43602 (AAD43602) T3P18.1	83	8e-15
O04365 (O04365) OMEGA SECALIN	83	8e-15
O48809 (O48809) F24O1.18	83	8e-15
O65375 (O65375) F12F1.9 PROTEIN	82	1e-14

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 34 to 361 of CT610: this corresponds to nucleotides 83630 to 83957 of the genomic reference sequence.

CT611
Nucleotide
Genomic coordinates:
Start: 88938
Stop: 85761 (SEQ ID NO: 218)

Amino Acid
MEGVTSIVAAAVPEVAILITDLMGGRNNKRSTYERIVGIVGESGDLLEAILDICNRNSYR
DELLEGETVVINPTGLLKEISLLMKKALDMNIKMKSNDDPVPFTTLDQNEQEFIGHLKSC
KKQDGPAYKDLIHRIYSGMFVMKNTRLMLDEIIRGNAGDAVEEKNALCEAYAEMISDMDL
IRIFLLLVAIKRDQNKKHRHMKSVIYEDVVVSLNTLKDVFHKEWYMWPFSALQVGTKIRD
ARTFSVLFGSDMHEGRNNDRIWENMAFSVTEAFLSGPSTNNHYNKGHLRMYAARPVYDAM
EYVPQELHHILFGTKIAKMIDIVYRYSIYNVPYLLAADTERVEEPKKSVMSPSGLIISPN
ASLLENTPLSLVSRHGIPSARKLGSFILEHENAENMHLEEAIAKCMVSQTLQEESWGESQ
AAMVYQPSDEVEVIQAHVTKILSGNTTNKTCGLCYADLDMKPKFFNCSHENMKASYDYFP
VHAFMDTFEARQETCSAKLCPDCTIKHLMYVYEKVSAGSEKLKDVFRCPCCGEYMVQFIG
RCHEFSSLFERAILAGENVDPEYIAANKLLITELIKRAEKCFYTVELLQAEFMEMCKMDK
DFALDKDSKFTVVDNRFRPPVKLFKMVEGETGDSKCSLICTQCLLPNVCDQPNEMEDIVT
VDVPPPVLPYPPPEQLEDYYFQDVEDAEFDDPPTDELVRYDTGPGLHKWPMRLSCGFLAS
NFVPPNEEVTNCRQAVSILKRTPEKKIRGWNPESPEGKVLLALANWHSTDRMPENMKGLL
NDISVIHNTRERFQNRVKVHYLNSVFGGFDDRDFEQVVGVSIPLIATYFYVYEKLNHESA
LGLWAKMFVKNLIGEMVLERPECVFHRAHSFVLHCVDRRALSGIRPNQGAKMEIVKQVNI
VRQNMTSESIKDPVFTVDEKRTLEWKVEKEGQEIKTVKCPKCKTPNIKLGGCITMTCYDC
SGRRDGYPTVFCWICEDEITNPDHILIDHKLLYSDCKSTKAALEKVYNCTLCCLALRKCS
DSYLSKQRGGGEEEEIEIYVMEDGFEFDVHTKTAVPTK
(SEQ ID NO: 219)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
AAF04637 (AAF04637) HYPOTHETICAL 84.4 KD PROTEIN	1495	0.0
BAA78677 (BAA78677) HFB30 PROTEIN	44	0.006
AAD21842 (AAD21842) ANDROGEN RECEPTOR ASSOCIATED PROTEIN 54	44	0.006
O94793 (O94793) HRIHFB2038 PROTEIN (FRAGMENT)	44	0.006
Q9XII0 (Q9XII0) F7H1.11 PROTEIN	41	0.042
YKZ7_YEAST (P36113) HYPOTHETICAL 63.6 KD PROTEIN IN YPT52-G	41	0.056

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 1 to 829 of CT611: this corresponds to nucleotides 85988 to 86816 of the genomic reference sequence.

Hit to public SBV sequence:
gi|6165655|gb|AF099142.1: CT nucleotides 1 to 2738 match nucleotides 8582 to 11319 of the public sequence with a 99% homology, a score of 5398 and an Evalue of 0.0

CT612
Nucleotide
Genomic coordinates:
Start: 91607
Stop: 89060 (SEQ ID NO: 220)

Amino Acid
MGSNQQQSFISKRNGTKQEISLEKIIKRIENACLPVNQYVPKLDKNAINPQELASHIMDR
LPATISFQEMDDFLADYAKTKIVDHPDFGKLAGRFICSNIHKNTKEWNSFSATTQKLRHA
IHPGTGKPASVVNDTYYENVMANAEILDAVIDYKMDYLFTCFGLRTLEYSYLIKIGSPTD
RKKRILVERPQDMIMRVAVGIHGSDIKSVIETYDLMSRHYFTHASPTLFNCGTVTPQLSS
CFLLGLQDDSIEGIYDTLKEAAIISKTAGGLGIHFHDLRAKGSPISSWSGTHPGLMAFLQ
IFNVSVKKVSQGGDKRRGAAAIYISDWHLDVKDFIDCRKNAGNEDLRTRDLFPAIWVSDL
FMERVKAGKNWSLMCPHECPGLSDVHGEEFKALYEKYEAEGKGKEVVKARALFDQINSAR
IETGTPYVCFKDTINRKSNQENVGIIKSSNLCTEIVQYSDSEETAVCNLASIAVNKFVKY
SPIPSLRPYVDYREMKRVVKIMTRNLDKVIDVNFYAVDKTRISNMKTRPMGLGVQGLADL
FFKLRIPFESEEAALINKRIFETIYYGALEASCEIAKEKGETYELFEGSPLSKGIFQFDM
GKENIKNRDIYFNSLPIHDWEQLRRDIMKYGVHNSMFVAPMPTASTAQILGNSESFEPLT
SNMYNRNVLSGSFQVVNEYVIRELIKLGEWNSVTKQRIMASGGSIQTLPNIPKSTKELFK
TVWEINPRTTLDMAIQRGMFVDQAQSLNLFVEEPELSKVRSMTMYAWEKGIKTLYYLRTK
GAARAVQFTVDKNVLQEVKKEAPSPVAAFSAPVREEEEEKKSSIVVPDPAAALLCSINNP
GACEMCSS
(SEQ ID NO: 221)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
AAF04636 (AAF04636) LARGE SUBUNIT OF RIBONUCLEOTIDE REDUCTA	1720	0.0
RIR1_SCHPO (P36602) RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE LA	807	0.0
RIR1_MOUSE (P07742) RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M1	804	0.0
RIR1_HUMAN (P23921) RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M1	803	0.0
AAD37491 (AAD37491) RIBONUCLEOTIDE REDUCTASE M1 SUBUNIT	801	0.0
RIR1_YEAST (P21524) RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE LA	796	0.0

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 1 to 845 of CT612: this corresponds to nucleotides 89225 to 90069 of the genomic reference sequence.

Hit to public SBV sequence:
gi|6165655|gb|AF099142.1: CT nucleotides 1 to 2547 match nucleotides 5913 to 8459 of the public sequence with a 100% homology, a score of 5049 and an Evalue of 0.0

TaqMan Primer/Probe Sets:
5'start=1327
5'stop=1348
3'start=1383
3'stop=1402
5'primer=GTCGGCATCATCAAGTCTTCAA (residues 1327 to 1348 of SEQ ID NO:220)
Tm5=58.78
3'primer=TGCACACTGCAGTTTCCTCC (residues 1383 to 1402 of SEQ ID NO:220)
Tm3=58.45
probe1=TGTCCAGTACAGTGATTC (residues 1365 to 1382 of SEQ ID NO:220)
probe1start=1365
probe1Stop=1382
direction1=Forward
Tm1=69.00
score1=1.99
length=76

CT613
Nucleotide
Genomic coordinates:
Start: 94397
Stop: 94175(SEQ ID NO: 222)

Amino Acid
MVIRLCFLESITCFVYGIMAPLSLDTNTDYLSHKKDTNKKIQMQINFIPYSNMHVYIAGV
YTFHEKKGLTYQQY
(SEQ ID NO: 223)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
O96794 (O96794) AMINOPEPTIDASE P	29	4.1
YA2G_SCHPO (Q09706) HYPOTHETICAL 157.7 KD PROTEIN C2F7.16C	29	4.1
O24567 (O24567) ESR3G2	29	5.3
AAC36183 (AAC36183) PUTATIVE PEROXIDASE	28	9.1

Comments:
Hit to public SBV sequence:
gi|6165655|gb|AF099142.1: CT nucleotides 1 to 222 match nucleotides 3447 to 3668 of the public sequence with a 93% homology, a score of 357 and an Evalue of 1e-101

TaqMan Primer/Probe Sets:
5'start=48
5'stop=65
3'start=169
3'stop=194
5'primer=TGGCATCATGGCACCACT (residues 48 to 65 of SEQ ID NO:222)
Tm5=57.92
3'primer=TCATGAAATGTGTACACACCTGCTAT (residues 169 to 194 of SEQ ID NO:222)
Tm3=58.55
probe1=CTTTGGACACAAATACCGA (residues 68 to 86 of SEQ ID NO:222)
probe1start=68
probe1Stop=86
direction1=Reverse
Tm1=68.82
score1=1.22
length=147

CT614
Nucleotide
Genomic coordinates:
Start: 129006
Stop: 127158(SEQ ID NO: 224)

Amino Acid
MEYIGEKNNNPVSNESVSEKELKLRSSFLMIGKKTSKYEQVMGVYEAIESIRQSELSEDT
FVVHVKKDKQLKFARGLKRLQELVEDDSLRIERISCAPPEPGHLFKDDAGHVTDEEWLAT
QEEDVRKINTIVKEKLKRKDKDFKFSQLYRYMSNSLSEAVEKKHDCMIISSDFLIGLGFS
TMNVTHALKSMERTMQKHGFKDMMVPLVEICHRTHYKGEYIANPIFKSHSSHCLIVPLFM
VAGVFARSAHPSAASIEMYLSTLAYAVILYSDEKQRQIREELARKNLQIKEELENQVEKT
TKVEKELETQVVKTTKVEKELETQVVKKEEYKNSYIETEQLFKVSEEQKESLRNVHKKSS
NATFRYDSGSCLVFSISSTEFYLLCRTDKSGSFETATENGLRYIFSPINKKRDTAGMRPR
LIMAVTGCDAPIACNDSIKHQNKFKVLKCNRSSIVFQTPPSDEDLKGIVQKVTGSDIRIF
MNDGTVYQDGQRIDISSPQELDEENMTQFEIEQQRKLHSMMENTSKIVTRYNKERHLTTK
EARTRNKTEKWFEKVKKREEQKKRENGEQSTSEQEQRGVKRTWENDNEFDSDVEEEEDGN
NTQEQQRVKRHAISV
(SEQ ID NO: 225)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
Q06166 (Q06166) MATURE PARASITE-INFECTED ERYTHROCYTE SURFAC	54	2e-06
O66878 (O66878) CHROMOSOME ASSEMBLY PROTEIN HOMOLOG	53	4e-06
GLE1_YEAST (Q12315) RNA EXPORT FACTOR GLE1	49	8e-05
O35788 (O35788) CYCLIC NUCLEOTIDE-GATED CHANNEL BETA SUBUNI	48	2e-04
Q14789 (Q14789) GIANTIN (GCP372) (MACROGOLGIN) (GOLGI AUTOA	48	2e-04
Q9ZU69 (Q9ZU69) PUTATIVE VICILIN STORAGE PROTEIN (GLOBULIN-	47	3e-04

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 2 to 976 of CT614: this corresponds to nucleotides 127217 to 128191 of the genomic reference sequence.

CT615
Nucleotide
Genomic coordinates:
Start: 130290
Stop: 129405 (SEQ ID NO: 226)

Amino Acid
MEYIGEQKLINLLDETPEEDELQLRSSFLMIGEKQYEKYEEVMSTFEAVETIRKSEFRDG
VFIVQLKENKHITFEGGLKELRELTGDNSLKIESLLSSIKPEKGHVILKNTSTTTDDEWL
ASQDKDVQEVNKLVKEKTRMLFRGFYFSPTYRYITKSLPQIPFGEKERFVVSTDFLIGLG
FSADDVMEKLIAIEGNMRKSGLKYTWVPVAEVCHLKKYKGDIVVNPIFKSYHSHCLVIPL
VYLGYMFSRNVQPPSLEVETYLLALAFAIDLYGREEMRKSCMRLCEDISEVKRG
(SEQ ID NO: 227)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
Q13779 (Q13779) APOLIPOPROTEIN B-48 (FRAGMENT)	36	0.34
APB_HUMAN (P04114) APOLIPOPROTEIN B-100 PRECURSOR (APO B-10	36	0.34
Q13788 (Q13788) APOLIPOPROTEIN B-100 (FRAGMENT)	36	0.34
P96470 (P96470) IGA-SPECIFIC METALLOENDOPEPTIDASE PRECURSOR	36	0.44
O28789 (O28789) SIGNAL-TRANSDUCING HISTIDINE KINASE	35	0.58
CAB55172 (CAB55172) HYPOTHETICAL 77.9 KD PROTEIN	35	0.76

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 1 to 725 of CT615: this corresponds to nucleotides 129499 to 130223 of the genomic reference sequence.

TaqMan Primer/Probe Sets:
5'start=296
5'stop=318
3'start=360
3'stop=383
5'primer=TTAAGCCTGAGAAAGGACACGTT (residues 296 to 318 of SEQ ID NO:226)
Tm5=58.14
3'primer=TGTACGTCTTTGTCTTGAGAAGCA (residues 360 to 383 of SEQ ID NO:226)
Tm3=57.87
probe1=CTACTGATGACGAGTGGC (residues 341 to 358 of SEQ ID NO:226)
probe1start=341
probe1Stop=358
direction1=Forward
Tm1=68.84
score1=1.84
length=88

CT616
Nucleotide
Genomic coordinates:
Start: 147517
Stop: 144748(SEQ ID NO: 228)

Amino Acid
MESIKEQQQQQPTVTFSEEPDQVYEFEDTTTTSAKKPTPSKAKFAAGRRMVSKQRRNTIR
SPHTETVEEVVGEEEEQQQQTPPEITPAEKKQQSLQELDALMGKVPAHLDVSVLAKSVAE
FLENDEDEDEELEKNKKAQKSVLFNSVMNSGRTELSPSTFCDGCVSKVKSAFEGKDLVSN
IVKVEGEAVKKTAIATDTTKLANLFLGCMNLQFHEHVTIETLNKKALDKGGPLFTLKLSD
AVYVDEMDLEKKRQIFGSNGDKSLFKELGGNYIDSAIKSTGLVMSTPSSSSTKKAGTHFK
TTNQIVEESVTESMRNGCCCFKNDKWLAKRESNLKSLNNTVFGEEDDEKSAYAYSDSEDE
DEDENEEEVDYDYNNETIESSVGNVIKNLIRKTIGLSDVEEEKEEGEQSEEEEEDSDDDD
DDASSVCSSSSSSSSVTVVAAAEEEEEEDEEDKDKDTATVVEDEDDKESVISSSSEDSEE
DEDDDGATSQCSEVVFGDVTECEFDESDGNPLYLASDNSFRPSASVTKYPQSEEEMDVSL
LSKNRSTPVCLSLCRHSSGCITNSFNMSTILKSLKLFPAGTEAAEDCVHIESTKKKDEDE
DEEDQGLDLQNSQYYSVLVDVDNLIIFSMGSTTYESSMVEVDYDKSFWSSFDKSVKPYCE
SKKSALINALCEDNVTAKVYATVHTLAIPFCESMPINHINNTTPYGSYKTFRISLPGNFS
GQHNDINNNWRSDMYTKMVENLLKREVVENKTHSRRYVRNLIVDGGVGENSGNYLKVHEN
NEDIFGSIEANSMSAKTAAAAFKNVAKKCDLIQTTTNDILTGPFKQYLIDYKYNSARKNI
IMEPCEGDETTAHEMKRAQDAYKQALHRAKITASSISLRGIWHEMITRDMNTTYNSMFMY
IPDFYKYVQVSPVNVSPLYMLD
(SEQ ID NO: 229)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
Q9YTL7 (Q9YTL7) ORF 48	85	1e-15
AAD56625 (AAD56625) NUCLEOLIN-RELATED PROTEIN NRP	77	6e-13
NUCL_CHICK (P15771) NUCLEOLIN (PROTEIN C23)	76	1e-12
GARP_PLAFF (P13816) GLUTAMIC ACID-RICH PROTEIN PRECURSOR	75	2e-12
IE68_PRVKA (P24827) IMMEDIATE-EARLY PROTEIN RSP40	75	2e-12
NUCL_MESAU (P08199) NUCLEOLIN (PROTEIN C23)	75	3e-12

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 476 to 1 of CT616: this corresponds to nucleotides 145115 to 145590 of the genomic reference sequence.

TaqMan Primer/Probe Sets:
5'start=1507
5'stop=1526
3'start=1554
3'stop=1575
5'primer=GAATTCGACGAGAGCGATGG (residues 1507 to 1526 of SEQ ID NO:228)
Tm5=59.36
3'primer=TGAAGCAGATGGTCTGAAGCTG (residues 1554 to 1575 of SEQ ID NO:228)
Tm3=59.21
probe1=CTACCTGGCTTCAGACAA (residues 1536 to 1553 of SEQ ID NO:228)
probe1start=1536
probe1Stop=1553
direction1=Forward
Tm1=69.02
score1=1.97
length=69

CT617
Nucleotide
Genomic coordinates:
Start: 148612
Stop: 147766 (SEQ ID NO: 230)

Amino Acid
MSPVISQQSSPSATSTAAARIISTANLRVLGVKNKEEKDEEEEQQEVEPEIIEPATDFEI
PFSPALTICIYINANRIHINSKGVCLNRKKIKPTSTINKNQDVPPELANASSYLVQTEHV
TDKFLSSHCSICNYNVNDGEYKSALSTTRNGDQPLMRKSVRYVPLNEDNVVVQKGTYYGT
TFIPEKTGRRILWFSHYKKSPRPITAKLCCLLETINSFNGSCSSSSSASSSSNAPGPIEE
FQVSSSIFFKKEECCPLQMKWVEQNELDAESPVLVLLMLAL
(SEQ ID NO: 231)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
Q9Z2U2 (Q9Z2U2) ZN-15 TRANSCRIPTION FACTOR	36	0.24
Q20150 (Q20150) F38B7.5 PROTEIN	35	0.70
O94002 (O94002) SEC12 HOMOLOGUE	34	1.2
Q20497 (Q20497) F47A4.2 PROTEIN	34	1.6
O13779 (O13779) HYPOTHETICAL 71.2 KD MEMBRANE PROTEIN C17G6	33	2.1
P93002 (P93002) REGULATORY PROTEIN NPR1	32	3.5

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 1 to 741 of CT617: this corresponds to nucleotides 147819 to 148559 of the genomic reference sequence.

TaqMan Primer/Probe Sets:

5'start=363
5'stop=383
3'start=446
3'stop=467
5'primer=CGACAAGTTCCTTTCATCCCA (residues 363 to 383 of SEQ ID NO:230)
Tm5=58.62
3'primer=ATCAAGGGCTGATCTCCATTTC (residues 446 to 467 of SEQ ID NO:230)
Tm3=58.15
probe1=CGGCTCTAAGCACAACAA (residues 428 to 445 of SEQ ID NO:230)
probe1start=428
probe1Stop=445
direction1=Reverse
Tm1=68.92
score1=1.92
length=105

CT618
Nucleotide
Genomic coordinates:
Start: 150145
Stop: 148675(SEQ ID NO: 232)

Amino Acid
MESVRDVKFYTFMNVLAEKAKKIQRLNKDKGWRTSINAEIGYGGARLMDVRFTGRKSMDE
LARCLYNCDGEYTTLRLVGSSAGNIIVYSLAFIMGIRGECCGFNVNNRLRMGKIIDRELF
YKITGLNFPETVKCTCDGVRAICDLFLEVAALQEHPAWHETKEVGKKQQQHFNEFGSQYP
GTKFNKRHKLSTKIIQQMFSEEKTMEQVLAFSEGTAASGFSDLYVEAPIQYVVNMYRAIS
NMEGRVGAMYNLSRVLILLCSRWEKKPGYKNDFYSKCEMYIGSKKIVDDESFIFTDLITG
DLVPLVRLAPSNEDIQRDVIRFNDSTDILMDSIDVRDVVLPVLSKIIWQNVSARLKLRNN
KSLSKLAKWKWNGMVSTHDNFDSNDYVIEHKRQLAADIMSDSLSKNHLPNFSKTITEYDE
KENKTTPLICWNYIFELSPMGKHLFPLEEVCGFYEASLPLITPWQLKVVQKKRGRQMVIY
GPRKRPRTQ
(SEQ ID NO: 233)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
Q64568 (Q64568) ATPASE (PLASMA MEMBRANE CALCIUM ATPASE)	37	0.28
ATC3_HUMAN (Q16720) CALCIUM-TRANSPORTING ATPASE PLASMA MEMB	33	5.4
Q12019 (Q12019) HYPOTHETICAL 559.3 KD PROTEIN	32	7.0

Comments:

TaqMan Primer/Probe Sets:

5'start=676
5'stop=701
3'start=823
3'stop=849
5'primer=GAAGCACCTATACAATACGTGGTTAA (residues 676 to 701 of SEQ ID NO:233)
Tm5=56.76
3'primer=GGAGCCTATGTACATCTCACACTTACT (residues 823 to 849 of SEQ ID NO:233)
Tm3=57.26
probe1=AGAGTAGGTGCCATGTAT (residues 733 to 750 of SEQ ID NO:233)
probe1start=733
probe1Stop=750
direction1=Forward
Tm1=69.06
score1=1.93
length=174

CT619
Nucleotide
Genomic coordinates:
Start: 169814
Stop: 165116 (SEQ ID NO: 234)

Amino Acid
MSTTQTQTIERPLPGKNNEDNSRLACLLAEGLQQQQQQQDGDSEISLPLVNAGTFACYDS
TLANLTEGRLGSETENAKIRVKIHPSVFIIETNKEMTIEEISTKSLNALVEKRAREARRF
SSLTEQKFPRGGGGCYSRKNERFIEGEINNIKLNMEETASSLERLAGLLPVVINIKDWTM
HDEKEIRLDLKGNDGMEELVNISHLNQEEWEMERLSSSIVLKDAYGVFYAHHGILDIVLT
TSRFTGKLLQHPVIFRLMDVKVWINTPLQIAFPDTSKNPNAKKILYQHPSLTRLRDLNDM
ASNSKSVSSIIIPELSKFNSTEFGMHYFTAQCFFGKNTNSLKDLVTRYYQLSFKNKPQPK
LYEPTATATAASSSSSTASLTTEQKEKIAQSILSSKGKSLGDVSSTLSKEYDENRKRTKR
QKTSTDTNIVPSGAPTSISMKNPVTCFFGPQYTSIMDCISEKTDWIEMHLFLTSLNDAEH
NKTLVVDRKSNVSEIHDSGRFLTFGQNNTTAFIPDVDIPTLKLILRDDSGESSAAIIASL
IYYNNVNLEGREFSNVSDAVVGLFSGGSAITVGDIAREIASIYNIGRESNCDSILFPGEP
ILAGRRSYGRQYRWYDPINCVVGLYRSCLETMTRNIMRGQPVKVDETAWMYMHQQVLQVV
LLPFFDCVLKSGVWAVKEARQLTDYIVREVLLKYTADPDQHKFLLFKKPVMDLIAKIVTH
YAVIHSAADNGGVCLAFPRDPPFIVENDTSLRYYTLTDTPQSILNGDNVAENLKSATSVA
SSPSSSSRYSSETPIRVVNLPVPTGRFLKMNKDLELFINVPLISSKEQKQQQQQTTATAP
FSSETISKSFLNYVPPKSLTRNVTYGQNIAEDGFLGLKNKGELVSYFKVVKNTERDDGIK
DMEIGDINNHQDDTGSLSSSSSSFVDGVRTSFSVDGKIEHVSAFLPGTTSQPTNLPVHAS
KQVKYSVKELGMETVFFEPLLSSAVLYEASKTKSTQHLSPMRIYKECVSPLSTGRIDIFP
SKVGTVAGTGFEFIWKVLQYDTGLPTTLERLSPKIPSVPISGEDSKMEVIAESGKGVQNI
IAIAADQLRGSNNIVGGGTRRAIQQQQQQQQQETQAVVPVNVPARFEPTFTEIELFLQNK
FRNVIATIISRMMMLVSNEEMKIIKEVCEHVSHIMVDGLYVALDPRKAIEEILERITAEQ
NGITIDTGNEGYGSLRYASSGRLFINDEASEEAAAAIGGGGALGTGRRVPVELRSILDKL
NTIGSTTQQQQQQQRQQRQANNNNTVPEDIKVHNEQMQKIRDSSLFTSKLLNYIRDDGRK
DRIKTNISETLKKYSRIPSYFIASKAQKPIPWKHTKDNINLNKIPEDLNFSPAQNLFVPV
NPRHILTDMQWLNCISIIETATRDSAIVMQSFQEQADKTTTQLEELLSQWNNIVSQVTDE
KSPAYVSSVKLEWLNNEASRIAAIRENSEKSKIVMGVQGKIVNIDELGIVAVARSIVDVD
FYIKMPNVWASRDWKNLIYYAVNIAATPLINNISRGIMAASQTSVLYDSSLALIAAEQAT
RNITM
(SEQ ID NO: 235)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
ST20_YEAST (Q03497) SERINE/THREONINE-PROTEIN KINASE STE20 (	46	0.001
YN23_YEAST (P53832) HYPOTHETICAL 52.3 KD PROTEIN IN MRPL10-	41	0.047
Q24523 (Q24523) BUNCHED PROTEIN, CLASS 2 ISOFORM (SHORTSIGH	40	0.11
NIT4_NEUCR (P28349) NITROGEN ASSIMILATION TRANSCRIPTION FAC	39	0.24
O62235 (O62235) F36F2.3 PROTEIN	39	0.31
MYSG_CHICK (P10587) MYOSIN HEAVY CHAIN, GIZZARD SMOOTH MUSC	38	0.53

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 234 to 1099 of CT619: this corresponds to nucleotides 165434 to 166299 of the genomic reference sequence.

TaqMan Primer/Probe Sets:
5'start=1920
5'stop=1941
3'start=2022
3'stop=2045
5'primer=GCCAGTGAAAGTGGATGAGACC (residues 1920 to 1941 of SEQ ID NO:234)
Tm5=59.57
3'primer=AGTTGTCTAGCCTCCTTTACAGCC (residues 2022 to 2045 of SEQ ID NO:234)
Tm3=58.24
probe1=CTTGGATGTACATGCACC (residues 1943 to 1960 of SEQ ID NO:234)
probe1start=1943
probe1Stop=1960
direction1=Forward
Tm1=69.03
score1=1.96
length=126

CT1020
Nucleotide
Genomic coordinates:
Start: 62990
Stop: 63659(SEQ ID NO: 236)

Amino Acid
MEWINQRTSREDLFNTYTGNAVIRSAAKQALAIEKHAAERRGEKAWTTSAAAAASSNFNN
VQQDYTDDDITQVSIANSVLNNPFLKRYAKLIDNLAISSLPPDIEDDVIIHTRDASNSTV
RVDGANIYFAIIDGDLCVYPKQYISDKVLCGSLNREKALFYNSSKNKWTYGCNLNFDIVD
AAIMKHPDYKEETTSTKHIRKILGIGASEKLNITHYLNYFIQ
(SEQ ID NO: 237)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
P75338 (P75338) MG307 HOMOLOG	32	2.7
Q80990 (Q80990) LATE MINOR CAPSID PROTEIN L2 (FRAGMENT)	31	7.9
Q18668 (Q18668) HYPOTHETICAL PROTEIN C47D12.2	31	7.9
Q80991 (Q80991) LATE MINOR CAPSID PROTEIN L2 (FRAGMENT)	31	7.9
Q80985 (Q80985) LATE MINOR CAPSID PROTEIN L2 (FRAGMENT)	31	7.9
Q02689 (Q02689) HYPOTHETICAL 45.6 KD PROTEIN IN COI INTRON	31	7.9

Comments:
TaqMan Primer/Probe Sets:
5'start=331
5'stop=354
3'start=379
3'stop=402
5'primer=CACACTAGAGATGCCTCCAACTCT (residues 331 to 354 of SEQ ID NO:236)
Tm5=57.74
3'primer=ACCGTCAATTATGGCGAAATAGAT (residues 379 to 402 of SEQ ID NO:236)
Tm3=58.84
probe1=CAGTCAGAGTAGATGGAG (residues 356 to 373 of SEQ ID NO:236)
probe1start=356
probe1Stop=373
direction1=Forward
Tm1=69.01
score1=1.98
length=72

CT1021
Nucleotide
Genomic coordinates:
Start: 69264
Stop: 76212 (SEQ ID NO: 238)

Amino Acid
MSDTGQMEENRPATQKRRPGDEEEEETGSSNVPYYANFGDDATYSMYTGEGKRGKFVLEP
PKERSVQRVQKPPKEKEEREQRSNVRTRRPGQEFEQKVLQDRSRERSEKLGQNLAEKGLQ
ERQKKYTPKVAQTMTKKIIRFREGGRKFKAPQQQTSDKGAATNVLEREEIEMAAEREQPV
EITGDTILGGLGEEDDEDMGEDELTIQHSSMAVSQPVQQIVVSSPIPPKPTRPAPDIPIQ
EDIVGKNISQLPPLPLDDYEDEEDEHLYEEVNDFLVAPPTAAAAASTRPPRPNIPPPPPP
VVAVADETLKNLASIAALEKEAEEQRAAAVERERVEEQRAAAAAAAAAAAAQREADEKR
EREAEEQRAAAAAAAAAAAQREADEKKEREVEEQRAAAAAAAAAAAQREADEKREREVEE
QRAAAAAEREILAQQLQEMKEQMRIKEEERRKELADKEEEKRRELAAKEEEKRQEILAKE
EQLEKLNFQLGTEITSKRALEQMLEEEKASRSRSAASAQLAIQAIEYEDELPQAVEPQGQ
LVPMDTDLYGKMYDLNKKLEVQNNTLTSAFEDVNKTNEQNQLVAQSLEKSAKAIEKLTSQ
KHLPVDDPAFMQRIITERDFSLKNLGNVYKRVLGVYFTLKRDLFKSKALITDKESRDLEV
RLTDVSTDLRANDLNTILERLDVSVNIRSGGTLYTKFTEADTALADQVPSRIEISNRSRS
ALLPFSSAGLDTNFTNSSDKYNEIVNQLSSINEAMNILKENIVPTLNQIKIDVTNLLTVS
SSRQYAIEERVYSDVSRMDSEIRKFLAIMNSKISPYFKGDWTDERQRSIADSISSQIKSN
DKIKESVATLHDINTTSRIRSNPLLHKSSVLSSPDFLNAVNDFRNFLDIQGGSQFTYDVL
SGQNIDDLSLASKTTEKVTELCLELSIILDVIHKNALSLNLPAITYPAGETSMEESGSLA
VDIRQEIGKNISDSSAELSRTLSEALQIFQQQQQQQQQQFQQQLLQQQQDQQNQQQLLQQ
QIEEQQRVQEQQQQQQRDQQQQEQQQREQQQQQQQREQQQQREQQQQQQQQQSDQFRQQL
LQQQQQFQQLLQQQGRRRGGDDGDEEREEREEGAEKDDCVRKVAESVATKYTADLTTLFQ
REENNFQSKIASAKLGTLVFATPPSPIMNLTKLREEYSTFTTQCFSKLTAENNSIMRIFP
ERIVEVCKSKNLNLMGKYLYIITTAQTEMEDRVKNILSGIFNQIEEFSNNVKQQQQQQAA
SASSTNPPPPSTPSTTPPVTSMQVCELDDQRTLEKAAIVEAITLANAVLQTTKSASAPST
AAEREIALKLENGKTSIRMEKVDLSSGATGVSDQQKWIDESTSKQELEDFIAEENFVETA
HNEMDIGLILDAKKNDPTRDANLRLVKPHGINVQSFPYYVLRTWLGETDILDEDTVHPEY
FRQYIDRNWKVEEHEREDTLKALGVSLSDTLAHIKDYYSPSVKNDASKSVPFALNTLLYN
IFAIDGGMISSLSRTAFIYRKFLRQSMTDKEVAQGPVRSQLCEATIASLFTACSNLLRSS
PLADKVEPRLQEKLAAAAAVDTSTGDMFRIRVCHLMYNFIVAYVNLCNNRINYTLNVLRA
SGLANKKVVAGKTTKGHTSSSHRFGSYDVTYDFSVLYKILQLQKQNISLLLEKGFNAWES
CVAAMAAFTADPSLSISDADQSILFPLEGGEIVIEKHENDAEKNVDMVQELWKETALTLM
AKELNSYYNWFIYSKDTDMEKLARVCRMIIGIVKAVLRLTNKAESLVDTNALSDIFKLPV
IPIDDTKTLAINIVVFTLNNVIKPWMVSFKQMFRQKDGGVSSAYFSFQNIQQQKHQQTAS
ILDAWACAPGKLTKAAHVFISGYENHIKLKKDDLLWGASMKFPADGRGTVVEGWAQQYNN
ESVLEDFTDFSIEVNAPASGLLIPPDPLLSSMFGKGNGGSSSSSSKDNTIIGKGGLILNR
QVVGQEQAPPINTSSDTKKIRRDANIEPIIGTPYSVIKASKGVSISVLDDFNEDSPEDFA
LKTSIINDAIREIGQRMTYTRPIFDHQTQKNIHYSSPKIILEGSDLKNGQRSGQSWAPSS
SSLTLASDWNLPSLELLYRELATKQVEKEEEEKSEREEDKGQKLNEKLSFVVNKAIGTIQ
QQHQYSERGGGMKRYQQHSADQASNGGIDDIELMNSKDATSMRKAKLALAVTNKIAAAAA
RDGENSSAKPSNFGNRLDEAINPGALLLRRGGGVRGGQTPQSSMLTMFRPGQTGGNSSWW
TTNTPLIQRTTSVGNNLVVLVPNLLDSHPPTFN
(SEQ ID NO: 239)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
O76853 (O76853) SRF RELATED PROTEIN	136	2e-30
AAD50121 (AAD50121) ADENYLYL CYCLASE	131	4e-29
O77033 (O77033) TRFA	120	8e-26
AAD46501 (AAD46501) LATENT NUCLEAR ANTIGEN	120	1e-25
O88542 (O88542) OPA-CONTAINING PROTEIN 1	118	4e-25
Q62006 (Q62006) OPA REPEAT (FRAGMENT)	118	5e-25

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 1 to 462 of CT1021: this corresponds to nucleotides 75184 to 75645 of the genomic reference sequence.

TaqMan Primer/Probe Sets:
5'start=3774
5'stop=3799
3'start=3851
3'stop=3872
5'primer=AGCTGCTTCAGCTTCTTCTACTAATC (residues 3774 to 3799 of SEQ ID NO:238)
Tm5=57.20
3'primer=CGTTGATCATCCAACTCACAAA (residues 3851 to 3872 of SEQ ID NO:238)
Tm3=57.20
probe1=CTGTTACAAGCATGCAAG (residues 3833 to 3850 of SEQ ID NO:238)
probe1start=3833
probe1Stop=3850
direction1=Forward
Tm1=69.00
score1=1.99
length=99

CT1022
Nucleotide
Genomic coordinates:
Start: 79064
Stop: 83375(SEQ ID NO: 240)

Amino Acid
MDFEGTTSSTPSKMSQLYSSVKKVAEHSFANLHDKATLASKVIKDLEGERKKMSTPKSSS
DGQKLDKAMLDDIINEYQAVKSTADNSIESTIKEIENVLESVRRTKIESEAKNSVTSSPE
KVFSVEDLEIYSKGRVCKGLKLNANCSRIGGKYAVSMSIKKHNVSSFENNNNQVFSEEPR
DCFMLETTYPLVGFETSTEDGNTYAVFLTGVGLERSLPKYVPVFDMNAGIQTLNMTGLRM
AKLPVLCMFGRTEYDNLEDFYITSIETQSFDEEENDARMRCHTEDLERKKRMNDAPAITP
HVAVYDYSGDGKEQLLYMITEYENTASWCNANGVVTSDSGFSNECAISDMNDLCCFADCI
DVTVNNEEHEERSMNIVVESDRRLFDASPSPIKTEEDGENSSSSSSSPTVPPPTPYEGNA
VVEGEEEEEEEIDEDESSKYEGSEDALVMKKLAKLSTMKQMRRVKNEPALKITSGGNNSSS
SINNEDDGDDDDAVDATALCPQTEATVKNSFMAPNDERTENILYETMQISLAKICNNPSS
MSSYRVFTNKLQECLNTMDDSIRRRPTIWTEESQQFAKGLLFDEVVTSIVAHQMAQDICK
SEIFGGMFNANSTNIKGKYEGQKKSLYGNKHISSSCFKTNTESNVNNALFAWVKSKLHSG
TVIPNVFSFKMASEKPSKMKRKRTSSASSSNDEHQEPSTKMMKNDEGEKVAQESSSPSSS
STPEQQQQAGHDKETINLIPLSFIKMPRSNVNGSASYLSEIFGQRLCGLSDASSTFKRMC
KTFEDLENEIMRSSFTRLTRYEREVTRLYEKCRSQAVDIEENEMDVLSHQGELFAEFLED
PIAYFEEVLENIKSWSLENVNTPKRKNKYAKVLVSVNAIRRTYEEYHAFSKFVPMFLFNL
IKRELEGDNYTHDVHFSSTCLWYLTVMTRNRICDVLQYINNNNNDNEETDIVEEEEEGEG
EEDKMEESMDVEQQKQVRKGGRKKGQKFNSIGDQVIRKFVKSLCENSMVVSIAINSLISG
ISWMNKKIPPGFLKDSSTINTLDEVSRFVFSDVKINRKINGTDDKYETVFGVSTRVDSHI
VGPFSIPVDFSSAGLDKASCGKLYVNTIDGKGILTISPKYDSLNDEDVDSTTTDKLEKDI
LHLSKHDTFFNINKNKVLPFYNISPSSSLTEKKKTKFNRKKISSGMSNNNGMCVQTPSSS
NSVSSVSSIVAPSSSVLALSCSLSSTKKKSIWNENMFLTSRNMWRCGFVVPPKLCSFIVN
HRHAVKLVAETAPKTKLCRNIIDRNRKIRFNGLKKVCKSVSAFTGESTYLLNKNMTATSP
SDLNLCIYTSSLNDPLYTCKLTHEEYQDGNALDDYGAVFVNYTFKSIKSCSSKDETADDN
AAAADDDGSTTSTSSSTDTDAAAIQDFMHVMIKKIDAMKDIRGKYKKSLAKKTKKH
(SEQ ID NO: 241)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
UBP1_YEAST (P25037) UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 1	50	1e-04
O97236 (O97236) PFC0230C PROTEIN	48	3e-04
CAB43859 (CAB43859) HYPOTHETICAL 85.2 KD PROTEIN	46	0.001
NSR1_YEAST (P27476) NUCLEAR LOCALIZATION SEQUENCE BINDING P	44	0.006
Q21000 (Q21000) SIMILARITY TO C. ELEGANS MYOSIN HEAVY CHAIN	44	0.006
Q18918 (Q18918) CODED FOR BY C. ELEGANS CDNA CM11B12	44	0.006

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 1 to 1010 of CT1022: this corresponds to nucleotides 82212 to 83222 of the genomic reference sequence.

CT1023
Nucleotide
Genomic coordinates:
Start: 93228
Stop: 94137(SEQ ID NO: 242)

Amino Acid
MVSSITHLSLLFVVAVVASVVFTTEGASVRVKRCAVSPCPDVIDPDHRCQGRLCRRSTRG
GDDDDDDDDGGTFDTVGSGILGRKKRAAPPPEDEEEDDFYRKKRAAPPPEDEEEDDFYRK
KRAAPPPEDEEEDEFYRKKRAAPPPEDEEEDEFYRKKRAAPPPEDEEEDEFYRKKRAAPP
PEDEEEDEFYRKKRAAPPPEDEEEDEFYRKKRAAPPPEDEEEDEFYRKKRAAPPPEDEEE
DDFYRKKRAAPPPEDEEEDDFYRKKRAAPPPEDEEEDDFYRKKRAAPPPEDEEEDDFYRK
KR
(SEQ ID NO: 243)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
Q18401 (Q18401) COSMID C33G8	113	1e-24
Q9YTL7 (Q9YTL7) ORF 48	98	6e-20
P73032 (P73032) HYPOTHETICAL 185.1 KD PROTEIN	95	7e-19
Q43687 (Q43687) EXTENSIN-LIKE PROTEIN (FRAGMENT)	88	7e-17
Q09085 (Q09085) EXTENSIN CLASS II PRECURSOR (CELL WALL HYDR	83	2e-15
O14686 (O14686) ALR	77	1e-13

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 214 to 1051 of CT1023: this corresponds to nucleotides 93435 to 94272 of the genomic reference sequence.

CT1024
Nucleotide
Genomic coordinates:
Start: 94623
Stop: 95742(SEQ ID NO: 244)

Amino Acid
MDNLKGEFVALKTDLTHYKTQLDRSILVFVDVVGRLYVIVNSEQTAKKEGLATRVAKQAT
EIQQFKDEINNKYNALTNTLDDIIYIFDHGGSFKRAKHKAIIEAREYSKPLRELECMFTR
IADMLTLTFMTVYTNIITEFRHSSEQATNSINVTLGRLFLCDDLCNQLPKEEEEEEDLKQ
KFITFHANLYMLDTRLKKDLIIFKDVIQQLHVILQKDTYAVKEGVAIRCAKQMNEISQYR
DNLKDNYNTFSNILNEIVYIFDHGGHFEEVKHKAITLTRNYLKTLMGLKCMFKRISEMLS
LTFLTVYTNVIAEFINASNISDREINNYLVQLVTCNELCNQLPKPKQYRPLSLIDNIAYF
SLSVQKHLSGFL
(SEQ ID NO: 245)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
AAF04635 (AAF04635) HYPOTHETICAL 43.2 KD PROTEIN	747	0.0
O96219 (O96219) HYPOTHETICAL 139.4 KD PROTEIN	39	0.051
O64554 (O64554) YUP8H12R.45 PROTEIN	39	0.067
TPR_HUMAN (P12270) NUCLEOPROTEIN TPR	37	0.20
Q99968 (Q99968) NUCLEAR PORE COMPLEX-ASSOCIATED PROTEIN TPR	37	0.20
O97291 (O97291) PFC0960C PROTEIN	37	0.26

Comments:
Hit to public SBV sequences:
gi|6165655|gb|AF099142.1: CT nucleotides 1 to 1119 match nucleotides 3220 to 2102 of the public sequence with a 100% homology, a score of 2218 and an Evalue of 0.0

TaqMan Primer/Probe Sets:

5'start=478
5'stop=499
3'start=576
3'stop=598
5'primer=TTGTGTGACGACTTGTGCAATC (residues 478 to 499 of SEQ ID NO:244)
Tm5=58.28
3'primer=AATCTTTCTTTAGGCGTGTGTCC (residues 576 to 598 of SEQ ID NO:244)
Tm3=57.55
probe1=TGCGAACCTATACATGCT (residues 558 to 575 of SEQ ID NO:244)
probe1start=558
probe1Stop=575
direction1=Forward
Tm1=69.00
score1=1.99
length=121

CT1025
Nucleotide
Genomic coordinates:
Start: 95824
Stop: 97369 (SEQ ID NO: 246)

Amino Acid
MDSCCLISRITPELAGKLTWIFIPENNFKIVQNSLPDDQVISQFRYFDHRHCYTFMEILM
ANIKIQDRKQNTTAICELTTGREGLLCRRTIPVFLGSEEKREELLGNLPEGAEIFRPREV
MQVIGTLLDKKLEIDDGIASVKAALCAGSSSLYLIMSHIVKMTFSAITNMKDINEEYFVD
FIFRHKQFLNPEFFKHLISLLKNSRKEHVAHLVRRLEHFLMLWTLSKMRFTEMEENYFPI
SSDSDYGICEKCARKTPKYKLRIFRERKCCDRCCRLYHQQPPPEVYNWDGKITQQSNKGY
INAGDEIIGMLNSNDKGKTFPPIPKMVVRRVVDGVYGQGTILSKILKFRQANIPTCLFVT
CNKCNRIFRLTILGPTRNILCPPCRKKSVAVNTQQKGENKPSFVQKGTKRLRVDTGSNKN
TLEKFCSWERFNTEVLLPWLGYTIESKWQNWESFLGYSSTRYKELWAFVNKQEISSMKDS
YIKIEDIDQLLRSILQDQKGVFETVCKIKSRDGL
(SEQ ID NO: 247)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
AAF04634 (AAF04634) HYPOTHETICAL 45.2 KD PROTEIN	689	0.0
STA5_MOUSE (P42230) SIGNAL TRANSDUCER AND ACTIVATOR OF TRAN	32	7.5
AAD20715 (AAD20715) PUTATIVE DNAJ-LIKE PROTEIN	32	7.5
CAB60246 (CAB60246) HYPOTHETICAL 80.9 KD PROTEIN (FRAGMENT)	32	9.9

Comments:
Hit to public SBV sequence:
gi|6165655|gb|AF099142.1: CT nucleotides 1 to 1545 match nucleotides 2019 to 477 of the public sequence with a 99% homology, a score of 3031 and an Evalue of 0.0

TaqMan Primer/Probe Sets:
5'start=672
5'stop=693
3'start=765
3'stop=786
5'primer=CCTTTCCAAGATGAGGTTCACA (residues 672 to 693 of SEQ ID NO:246)
Tm5=57.77
3'primer=ACGGAGCTTGTATTTGGGAGTT (residues 765 to 786 of SEQ ID NO:246)
Tm3=57.84
probe1=TCCAGCGATAGTGATTAC(residues 721 to 738 of SEQ ID NO:246)
probe1start=721
probe1Stop=738
direction1=Forward
Tm1=69.03
score1=1.96
length=115

CT1026
Nucleotide
Genomic coordinates:
Start: 97547
Stop: 98789 (SEQ ID NO: 248)

Amino Acid
MESIKLFTVAGLNMEQANQVAEEIKSEYKTEEEKRIAQEVFDKFTKKLIMQVDTSKHLLT
RENPNRFVSRPIVHEDLWEMYKKEVACFWTLEEIDFERDPKDWEKLTQDEKDFILQILAF
FASSDGIVIENLTTRLRQVAQIPEARSFFDFQVGMESIHGNVYGELIDRLVPDEKDKAIL
FNAAQHFPAIKKKEQWAINWMQSNNDLAELIVAFAAVEGIFFSGAFASIFWIKNRGILPG
LTSSNEFISRDEGLHRDFACMLLKKGFVDTPSRERILEIVTEAVRIEQEFLTVSLPVKLV
GMNCKLMSQYIEFVADKLLVEMGLEKHYNVTNPFPFMDNISLENKTNFFEKRVAEYQRAQ
VMASINKIKKDQQTQETGSPLPILTAPPPVSSSSSEQEDVEDGVGDYISYDDF
(SEQ ID NO: 249)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
Q9XYN8 (Q9XYN8) RIBONUCLEOTIDE REDUCTASE R2 SUBUNIT	388	e-107
RIR2_HUMAN (P31350) RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M2	381	e-105
RIR2_MESAU (Q60561) RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M2	381	e-105
RIR2_MOUSE (P11157) RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M2	378	e-104
Q27124 (Q27124) RIBONULEOTIDE REDUCTASE SMALL SUBUNIT	377	e-104
RIR2_BRARE (P79733) RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M2	376	e-103

Comments:
EST confirmation of the predicted transcript:
An isolated EST has sequence identity to nucleotides 1 to 959 of CT1026: this corresponds to nucleotides 97786 to 98744 of the genomic reference sequence.

Hits to public SBV sequences:
gi|7672988|gb|AF144620.1: CT nucleotides 1 to 1242 match nucleotides 1 to 1242 of the public sequence with a 99% homology, a score of 2454 and an Evalue of 0.0;
gi|6165655|gb|AF099142.1: CT nucleotides 1 to 299 match nucleotides 299 to 1 of the public sequence with a 99% homology, a score of 585 and an Evalue of 1e-169

TaqMan Primer/Probe Sets:
5'start=642
5'stop=663
3'start=706
3'stop=727
5'primer=TGCTGCAGTTGAAGGAATCTTC (residues 642 to 663 of SEQ ID NO:248)
Tm5=58.19
3'primer=AGGTGAGACCAGGCAAAATACC (residues 706 to 727 of SEQ ID NO:248)
Tm3=58.13
probe1=TTAGTGGTGCATTCGCAT (residues 665 to 682 of SEQ ID NO:248)
probe1start=665
probe1Stop=682
direction1=Forward
Tm1=68.98
score1=1.98
length=86

CT1027
Nucleotide
Genomic coordinates:
Start: 98874
Stop: 99789 (SEQ ID NO: 250)

Amino Acid
MNLLPIFLTTFFVAVDACSCSTICLLPDGKKQPLVFDSVLEEVVYPTDVCGPKGAGELFT
GVDLLTLCIGGKNNGGEWSGKGPCPRINNAVVERDYSLDEEDCKGFRKGFRIPGTDHFHT
VFSLCWVDRDMHAKWVRNKINPGIVTDDEDLVDSGIRTKFKYSSKIFGKGFNPRPLYSLD
YQERIKILKSHFNKRTGNFFARGHLAPAGDFFLASERWATFALENAVPQIQNHNNGEWKD
IENRARTTPGAAWAETGPIFYQHKKKEYLDKKKKYIPIPHALYKIVYDKNNKELFRVQSD
MSWK
(SEQ ID NO: 251)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
CAB55635 (CAB55635) DEOXYRIBONUCLEASE I PRECURSOR (EC 3.1.2	59	6e-08
Q9Y2C4 (Q9Y2C4) ENGL-A	48	7e-05
NUCG_MOUSE (O08600) ENDONUCLEASE G PRECURSOR (EC 3.1.30.-)	45	0.001
NUCG_BOVIN (P38447) ENDONUCLEASE G PRECURSOR (EC 3.1.30.-)	45	0.001
O73911 (O73911) K123 PROTEIN PRECURSOR	43	0.004
NUCG_HUMAN (Q14249) ENDONUCLEASE G PRECURSOR (EC 3.1.30.-)	42	0.005

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 1 to 808 of CT1027: this corresponds to nucleotides 98914 to 99720 of the genomic reference sequence.

CT1028
Nucleotide
Genomic coordinates:
Start: 103891
Stop: 104680 (SEQ ID NO: 252)

Amino Acid
MSLAVTEDYGHNEKLIKRLQTSVYHTPLLGADHVMKSISDYIISRRFMNYTNLLKQVEYV
FDEETGAVIANICLLKILERCAQKGGIYDAPEDVAFFNSKMGEVTRLFTIIGGRPNMTVR
VNFKHGQTNNPAYGYLTDDNDTTTVTPPVTPPPSPAARRSPFFTRTLISESSSVDHYVLM
HDNPKRSSFKVYDIHAETFPHKAPSVPTFPPKTSFEISDVTLDCSMEIFSRDRDVLDNVH
DYIANDPVPFLVDVVHRGSSLR
(SEQ ID NO: 253)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
PAXI_CHICK (P49024) PAXILLIN	36	0.39
Q24459 (Q24459) POLYCOMBLIKE NUCLEAR PROTEIN	35	0.67
LA17_YEAST (Q12446) PROLINE-RICH PROTEIN LAS17	34	1.5
Q14676 (Q14676) KIAA0170 PROTEIN	33	2.6
Q94399 (Q94399) ZK265.2 PROTEIN	32	3.4
O88699 (O88699) HOMEODOMAIN PROTEIN	32	3.4

Comments:

TaqMan Primer/Probe Sets:
5'start=390
5'stop=413
3'start=457
3'stop=477
5'primer=TCCTGCCTATGGTTATCTCACAGA (residues 390 to 413 of SEQ ID NO:252)
Tm5=58.77
3'primer=TCTTCTTGCAGCTGGAGATGG (residues 457 to 477 of SEQ ID NO:252)
Tm3=59.15
probe1=CCTCCTGTTACTCCTCCT (residues 439 to 456 of SEQ ID NO:252)
probe1start=439
probe1Stop=456
direction1=Forward
Tm1=68.94
score1=1.94
length=88

CT1029
Nucleotide
Genomic coordinates:
Start: 104759
Stop: 107330 (SEQ ID NO: 254)

Amino Acid
MASTSSSTKKRVHEEDENLIPQPKKKKSKKVLPFPVDKYRAVDKKVVNLIHKILDQEKDH
LSSTELQMITECNGAREDLLKHLLDEGEFNPTIIEVVSSMPIETIYEILSSSADDKKFVQ
ISLSMLIHILFFADKGTMWVSNACVQNVLGNDYKVEFENIRKKYLILEDLLNGVSNHWSE
HGPLSHMLHSSIPIVQDMLLNRLVRYFSTYDGDAQFDISFIINSVLWGIDKSVLNELTQL
ISRGVFIVSYVPMRVRTPSKDSNRPQNTPSQNMSALGMKLNTFSSRISVYRNNTFKKLTE
LVHNFDYGSKDASSSSPPPPSLSDSVNTFVRLYTNYDIFLKVISDWKMPYGFFKKTFDVL
YSKGLMTLSVSEYTLKKELVTFLRALKEREILIYKMEKRDIICILKKSLFGFNFRCLKQL
LPLFKHFLKIEEVKHIARFVFRDYSLMCKTQKDLQSFPAIQSASLFMEEFPWLAKTWIDD
DDDEGGKGHTLLTFAIVHRYPLISQLISHPILKSLVNTTCRDKHFTPLMHLANTSIMYQC
NTLLCLIINGAKPEFINKFNENVLHIAIENVNYGVITELRGTLSSEQIEKMVNVRRMMDN
TTPLMIALARENIVLAQLFDGLYKPKIKVRFGSSKRLRIPEFVLLKGLKESVAYLETRNI
SYDINIIKDAVMDNSLFEEEYEIAAAGLRGNNCDPEADEKTMNTWNFFTKNSTKWASSIF
QKNRQKFVKIVDGMNRTYEDSECAICLDSLDGDLPSGRTTCGHCFHNVCWLSLIRMSGPN
NGSRARGGGIKCPSCRQVTCLGKRLGVADYDIETEEERDTKNVVPSVEEGRREWRKIGVD
RYEFLVGGVWTNEIKL
(SEQ ID NO: 255)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
Q9Y577 (Q9Y577) RING FINGER PROTEIN TERF	43	0.007
AAD27914 (AAD27914) T23O15.13 PROTEIN	40	0.058
AAD56722 (AAD56722) AUTOCRINE MOTILITY FACTOR RECEPTOR	40	0.076
Q9WV59 (Q9WV59) RING FINGER PROTEIN TERF	39	0.13
O82239 (O82239) F17A22.9 PROTEIN	39	0.13
RO52_MOUSE (Q62191) 52 KD RO PROTEIN (SJOGREN SYNDROME TYPE	38	0.22

Comments:

TaqMan Primer/Probe Sets:
5'start=1406
5'stop=1425
3'start=1491
3'stop=1514
5'primer=AATTCCCTTGGCTTGCAAAA (residues 1406 to 1425 of SEQ ID NO:254)
Tm5=58.29
3'primer=TGGCTTATTAAGGGATATCTGTGC (residues 1491 to 1514 of SEQ ID NO:254)
Tm3=57.50
probe1=TTGGATCGACGACGATGA (residues 1428 to 1445 of SEQ ID NO:254)
probe1start=1428
probe1Stop=1445
direction1=Forward
Tm1=68.95
score1=1.95
length=109

CT620
Nucleotide
Genomic coordinates:
Start: 172439
Stop: 171509(SEQ ID NO: 256)

Amino Acid
MDNLITNDNIILVTFLSGLAVGCSMTIGLALAMNMLVKCIDRTTTCISCSPWEKNKNKKN
RNGSNTESSFISHVRFNTPDKDLDISEPMLKSTTYDLANVTPQVTKLVTFSGPTYASPPT
PRPVANTPQQQPTSTNKEEESVYMPMSSCSSSFSSDNSLPLPTPPPSPPRSNGGDYVSYV
NGRHLKLPSNPPSPIFNIKNEEGEDDNVEEHVYEYVPEVPQQSPSIQKCIQELKEMKHKK
NTLTRSSSNNNNNAPRITQVTFKKFPPNNNNMWENHVYGNTTIVSSTPSPTFIPSPKSII
RKLSFKRKQ
(SEQ ID NO: 257)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
Q24035 (Q24035) ENA POLYPEPTIDE	46	4e-04
Q41805 (Q41805) EXTENSIN-LIKE PROTEIN PRECURSOR	43	0.002
Q40786 (Q40786) ARABINOGALACTAN-PROTEIN PRECURSOR	43	0.003
Q9XZU9 (Q9XZU9) LARGEST SUBUNIT OF THE RNA POLYMERASE II CO	42	0.005
O36428 (O36428) GLYCOPROTEIN PRECURSOR	42	0.005
YHC4_YEAST (P38741) HYPOTHETICAL 80.1 KD PROTEIN IN SNF6-SP	42	0.005

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 665 to 1 of CT620: this corresponds to nucleotides 171494 to 172158 of the genomic reference sequence.

TaqMan Primer/Probe Sets:
5'start=494
5'stop=513
3'start=558
3'stop=578
5'primer=CGCCATCTCCACCTAGAAGC (residues 494 to 513 of SEQ ID NO:256)
Tm5=58.49
3'primer=GAAGGTGGGTTTGAAGGAAGC (residues 558 to 578 of SEQ ID NO:256)
Tm3=58.68
probe1=GGCGGTGATTACGTGTCA (residues 517 to 534 of SEQ ID NO:256)
probelstart=517
probelStop=534
direction1=Reverse
Tm1=69.00
score1=1.99
length=85

CT621
Nucleotide
Genomic coordinates:
Start: 173054
Stop: 172505 (SEQ ID NO: 258)

Amino Acid
MGESIFDAVSLATNNPKKSNSRNKKLLRELKNMRKDFPSTFLQCRMIDFHFSGDIIDKHY
CHSVNVPDVVPNTIFAVFLPEEDRANNPGLYDSIEGVCITVEQGELCIINKSSVHEFNIL
VSLHKDLFGEDILDGIETASREESRSIHLYLEAGQSIRTPIPRPEGTNTVNYTIVFSNQV
TV
(SEQ ID NO: 259)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
O88632 (O88632) SEMAPHORIN IV ISOFORM B	34	0.54
O88633 (O88633) SEMAPHORIN IV ISOFORM A	34	0.54
O29244 (O29244) ABC TRANSPORTER, ATP-BINDING PROTEIN	34	0.71
O54948 (O54948) SEMAPHORIN IV HOMOLOG (FRAGMENT)	33	1.6
Q13275 (Q13275) SEMAPHORIN IV PRECURSOR (SEMAPHORIN III/F)	32	2.7
INA9_MOUSE (P09235) INTERFERON ALPHA-9 PRECURSOR	32	3.6

Comments:

CT622
Nucleotide
Genomic coordinates:
Start: 183817
Stop: 180274 (SEQ ID NO: 260)

Amino Acid
MEAASNLRITEGAGVLDIDNEDDINNNVDYSNLYEDEEDEEEMNEDEEEEEEEDYEDEDE
DTGVRNGRNKDPPSSKKQSKFVRDVTNDMYDDDDEEEEEEEEEEDEEGEEGGEYDGNLED
EEEEGDEYEDDNEGEGEEDEADPALLALAAQQEDATIIPENQWKSIVNTPSPVGPNRQVL
PMLNFLLENVNAMGGSAGEEQKNKEDDNQQIEPVEEEEDEEEEEQEEEEEEEEEQEEEEE
EKEPIEQEKNEPEKDEDAIENESVHSHRVESSPMSEGGNDDGMDYFFSSIAGGGNDNEED
EEEDEEEGEEEEEEEPAQKSEEHVETKESVQSHTEYIEEEEEYEEYEDESRHTLEDEEIS
TMHQFNNAPRVRRSPPPDIQECEDAVVFPPIMKETDILPQIKEPSPKAPRMFSILGSGGE
EQYDQLNDIAPPPVPSIVTFPPDNEMGEESRDIMDQDSMLMPPPPPPPPPPPHQPPQLKP
TNILLPPPPPPPTNQSLFSNNNNNPSFLSTVVGKVNNTLGGKEAEERLHKTMESIILKTR
VKTLLETTKNLQCSELVKVVFQDPENPVKPSEKVMERLKNIIAAELTMKAFLDSAAVTDI
KSAELFRKTNEKLELFQRKQIMSNPLFSAAYASTYIMGERASKIRPSTPAPSLKKVESIS
ELNEDETSMSSSAGGVCAEGDESIAGGGGGGGGGGEVVEHSSFYSNQTQANLHMELINI
LKEDDDNQPCQTYKLGQRLAFLNNLISFKTSSAVSWSRLVNMLSDIVTKASVALFGDTNK
AQEDFEKHQTETNDVSDLSTSSKLKQMSKESANIMEEMGLGSIGAEICFGAISTIIEKHI
NKLCMDVGRLTIFLNIPIVLLNWPKEFTLSKDYKVLLLDSISSCSSKMAVPPIYVLNSIQ
FDKAVDEEDEDGNGSEAEKRSEDGNMFSEKDKKEAIRRVYDNIRYGDSNDRTSLNHFFGD
AYSGVSNNNSKNSMFDLQTQGGGRFGVAYSAGSSIIEHRSPIFDNALNTLVNFMDKRKHL
LSAVVIKLLKKAKLSIEVYCIKYKLNQASEKYNKKGKHGKSTSVVPMRNLMYRPSKNQDV
SPSTPAAATAMDVPSSVSSHVGRKRTFSFSNDINSNMSSASSVYIDQESSTPSRRRTFMD
LLNNKSSVNSLAKQVKRMKHTKYYNSSSNSEDDDEDDQYE
(SEQ ID NO: 261)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
Q9YTL7 (Q9YTL7) ORF 48	154	3e-36
O40947 (O40947) ORF 73	148	1e-34
Q98148 (Q98148) ORF73 HOMOLOG	138	3e-31
AAD46501 (AAD46501) LATENT NUCLEAR ANTIGEN	136	1e-30
VG48_HSVSA (Q01033) HYPOTHETICAL GENE 48 PROTEIN	133	6e-30
Q91255 (Q91255) NF-180	130	5e-29

Comments:

TaqMan Primer/Probe Sets:
5'start=1940
5'stop=1962
3'start=2039
3'stop=2058
5'primer=CGACTCCTGCTCCTTCTCTTAAA (residues 1940 to 1962 of SEQ ID NO:260)
Tm5=57.98
3'primer=TCCAGCAATAGACTCGTCGC (residues 2039 to 2058 of SEQ ID NO:260)
Tm3=57.66
probe1=GTGGAGTATGTGCTGAAG (residues 2021 to 2038 of SEQ ID NO:260)
probe1start=2021
probe1Stop=2038
direction1=Reverse
Tm1=69.00
score1=1.99
length=119

CT623
Nucleotide
Genomic coordinates:
Start: 196292
Stop: 195506 (SEQ ID NO: 262)

Amino Acid
MSNGATISDERLILILDKIVERRGVSNLSELLIHPITKHINELLKNTVRHGDRVYMKDAE
LDVRSRLEDIKKDCVLKAIEKQGIDVRQIITDYLAKRKLTQNLVHWYRPPISCTDIDEKI
QQETGQVGRCSVATYNLRIGGDDGEFTRYDFSIPLGDFKITAKLFRSINDEDVDAVILVS
RSDVVNDVLSFEAFNRTGERVVIFFNVIVEGKSKDIDIVCKSRYKHTHILNGESATYAVK
RIKRGDTRDDILFAITAFKEE
(SEQ ID NO: 263)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
PYC1_YEAST (P11154) PYRUVATE CARBOXYLASE 1 (EC 6.4.1.1) (PY	33	1.9
BAA85008 (BAA85008) ORF3P	33	2.5
BAA85073 (BAA85073) ORF4S	33	2.5
PYC2_YEAST (P32327) PYRUVATE CARBOXYLASE 2 (EC 6.4.1.1) (PY	32	5.7
O27375 (O27375) ADENINE PHOSPHORIBOSYLTRANSFERASE	32	5.7
Q88444 (Q88444) GLYCOPROTEIN PRECURSOR	31	7.5

Comments:
5'start=282
5'stop=304
3'start=383
3'stop=402
5'primer=GGCTAAACGAAAACTAACGCAAA (residues 282 to 304 of SEQ ID NO:262)
Tm5=58.58
3'primer=CGTAGCAACACTACACCGCC (residues 383 to 402 of SEQ ID NO:262)
Tm3=57.92
probe1=CCAATATCTTGCACAGAT (residues 328 to 345 of SEQ ID NO:262)
probe1start=328
probe1Stop=345
direction1=Reverse
Tm1=68.97
score1=1.88
length=121

CT624
Nucleotide
Genomic coordinates:
Start: 195503
Stop: 194651 (SEQ ID NO: 264)

Amino Acid
MSSNGDEPAVTEAEIASVEAQLGAAHHDNSWITRKSDQLKYRLGAIAYSVAKNASIKYIE
DQVRQEINSHLTNVMTFEHLYEDAFNPVICEAIFEKGIPVVMEKVYDVNRRIMEPREDFI
TEILKEERWRRYIPGFYHTSFSFKYNTIAFTDSSTSFSVPINDKHMLSITPPGAAQGDLI
DLSLSFKIDSSAKTLTLEFNRKSTFAGIVNRPKSVVILSNLRNSDSSDNIGDYLKRNDPI
YISHDTNGIINPSEDSASLITIHMPEIENASDDLYIDFNLFVF
(SEQ ID NO: 265)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
Y687_METJA (Q58100) HYPOTHETICAL PROTEIN MJ0687	36	0.42
Q9Y717 (Q9Y717) CAGCR3 PROTEIN	33	2.8
Q83457 (Q83457) FIBRE	32	4.7
CAB53329 (CAB53329) PUTATIVE FORMYLTRANSFERASE	32	4.7
PGK_LACDE (O32756) PHOSPHOGLYCERATE KINASE (EC 2.7.2.3)	32	6.2
Q9XEQ1 (Q9XEQ1) TNP2-LIKE PROTEIN	32	6.2

Comments:

CT625
Nucleotide
Genomic coordinates:
Start: 194629
Stop: 193327 (SEQ ID NO: 266)

Amino Acid
MALSNNGGIYIVFAVIVLVIGASIALFFAISGVGKGTLHSNAKTKKSKKYKLDSKYTDDD
EKTDDDNNNNGGGGGGTVDVINETALQRQTREHFARTLEKAEDEFFTKLADQEFDTYKSE
NVWLIKDKITDGKVSIPEGDINVPDVGQAIADENLFDLIGTNHDEVKETMDEVVAQKSTN
ITYEQLVIDLTNILLFGTVTVDPSDENGDESLQRSTDPDAEMVMLTTTPSSQLARQQQPP
QPTPDYLARYSKELVINNIRGGFISDRDMRTWQGRMSVHVNMKQRTFNVISAATNLDSLQ
VGLEPVLQKQGRAAVGGRIEKARIEFSFVVEGNRVRVYATNKTEDCFCSLLPNCYNVKKA
SDYWISSASTAKEKTYLFIANKNDETSFFYNFEEGVEEIDLDIFMTIDCAPNLPFIKNLP
RPITDNNIMVALS
(SEQ ID NO: 267)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
O96148 (O96148) HYPOTHETICAL 57.8 KD PROTEIN	38	0.14
TRI1_ECOLI (P14565) TRAI PROTEIN (DNA HELICASE I) (EC 3.6.1	37	0.31
Q43423 (Q43423) CYSTEINE PROTEINASE (FRAGMENT)	36	0.40
O15696 (O15696) ORNITHINE DECARBOXYLASE	36	0.69
MIX2_XENLA (Q91685) HOMEOBOX PROTEIN MIX.2	36	0.69
BAA84604 (BAA84604) MYOM PROTEIN	36	0.69

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 351 to 1 of CT625: this corresponds to nucleotides 193270 to 193620 of the genomic reference sequence.

TaqMan Primer/Probe Sets:
5'start=651
5'stop=669
3'start=729
3'stop=748
5'primer=CCCAGACGCAGAAATGGTG (residues 651 to 669 of SEQ ID NO:266)
Tm5=58.66
3'primer=ACCGGGCAAGGTAATCAGGT (residues 729 to 748 of SEQ ID NO:266)
Tm3=59.29
probe1=ACAACAACAACCTCCTCA (residues 705 to 722 of SEQ ID NO:266)
probe1start=705
probe1Stop=722
direction1=Forward
Tm1=69.01
score1=1.98
length=98

CT626
Nucleotide
Genomic coordinates:
Start: 228196
Stop: 227989 (SEQ ID NO: 268)

Amino Acid
MSDMTRNIIVGLAVVVIALSMVAFMLSVTPALTGFLLGLGVSALGVTLFGCPTMKSPGGG
NATINPVA
(SEQ ID NO: 269)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
SUGE_PROVU (P20928) SUGE PROTEIN HOMOLOG	32	0.35
Q48546 (Q48546) INTEGRAL OUTER MEMBRANE PROTEIN	32	0.35
O86349 (O86349) HYPOTHETICAL 27.4 KD PROTEIN	31	1.0
Q9Y9X7 (Q9Y9X7) 604AA LONG HYPOTHETICAL CARBON STARVATION P	30	1.8
O69867 (O69867) PUTATIVE TRANSMEMBRANE TRANSPORT PROTEIN	29	4.0
O26370 (O26370) HYPOTHETICAL 5.9 KD PROTEIN	29	4.0

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 1032 to 768 of CT626: this corresponds to nucleotides 227951 to 228215 of the genomic reference sequence.

TaqMan Primer/Probe Sets:
5'start=60
5'stop=80
3'start=151
3'stop=173
5'primer=CATGGTCGCTTTCATGCTTTC (residues 60 to 80 of SEQ ID NO:268)
Tm5=59.30
3'primer=CCTGGAGATTTCATAGTGGGACA (residues 151 to 173 of SEQ ID NO:268)
Tm3=58.94
probe1=TGTTACTCCTGCACTTAC (residues 81 to 98 of SEQ ID NO:268)
probe1start=81
probe1Stop=98
direction1=Forward
Tm1=68.95
score1=1.95
length=114

CT627
Nucleotide
Genomic coordinates:
Start: 234330
Stop: 233778 (SEQ ID NO: 270)

Amino Acid
MFQKWFESFLDSSRPRYLDTTCVCSVYSYFSPCRKHIKFSTSHSHEGIKIHPPSILNHNT
SSPTSGKMCNHHHKRLYLSTDDHTRWYDKNTSCIYLEDIGGVQFMVYEFHLTPKNNQLFS
FPVHLQIHNRNTEKTSLLVFENEEDMRVRNIHPKSKILIPVSKDTVLVENGFRYKVKIVL
SNK
(SEQ ID NO: 271)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
TRBH_ECOLI (P19381) TRBH PROTEIN	31	6.4
BCL6_HUMAN (P41182) B-CELL LYMPHOMA 6 PROTEIN (BCL-6) (ZINC	31	6.4

Comments:

TaqMan Primer/Probe Sets:
5'start=187
5'stop=207
3'start=233
3'stop=253
5'primer=CCCACCAGTGGAAAGATGTGT (residues 187 to 207 of SEQ ID NO:270)
Tm5=58.36
3'primer=TCGTATGGTCGTCAGTGCTCA (residues 233 to 253 of SEQ ID NO:270)
Tm3=58.89
probe1=CACCACAAGAGATTGTAC (residues 214 to 231 of SEQ ID NO:270)
probe1start=214
probe1Stop=231
direction1=Forward
Tm1=68.98
score1=1.98
length=67

CT628
Nucleotide
Genomic coordinates:
Start: 240139
Stop: 239455 (SEQ ID NO: 272)

Amino Acid
MDSLISKLENIFSIAEQDFFNADSMFMQTMLLPTDAMFTDCESPLYKNKSGGKNIVTDVG
ESVLSSSSDEKMSFKVLSHVLRRFPVLLHCNYKQTNTPLWKELYKHGKFALLGDLVLFSN
PFHPNIPAMPFDKSPICDTTGKSIIMSEVMTKELLYKLADKDIGQFFAVLNVTNPITGDS
FLHYFAGGNTMRDGEGDKICTSADVLRIIAEITIQKTGKMPYELMKK
(SEQ ID NO: 273)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
SYT_HAEIN (P43014) THREONYL-TRNA SYNTHETASE (EC 6.1.1.3) (T	39	0.028
SYT_ECOLI (P00955) THREONYL-TRNA SYNTHETASE (EC 6.1.1.3) (T	38	0.049
CDR1_SCHPO (P07334) MITOSIS INDUCER PROTEIN KINASE CDR1 (EC	35	0.55
Q55626 (Q55626) METHYLENETETRAHYDROFOLATE DEHYDROGENASE	32	3.7
ERG2_SCHPO (P87113) PROBABLE C-8 STEROL ISOMERASE (DELTA-8-	32	4.8
Q85056 (Q85056) SEGMENT 2	31	8.3

Comments:

TaqMan Primer/Probe Sets:
5'start=246
5'stop=267
3'start=288
3'stop=305
5'primer=GCGATTCCCTGTCCTACTTCAT (residues 246 to 267 of SEQ ID NO:272)
Tm5=58.22
3'primer=TCCTTCCACAGGGGCGTA (residues 288 to 305 of SEQ ID NO:272)
Tm3=58.60
probe1=CAACTACAAGCAGACGAA (residues 270 to 287 of SEQ ID NO:272)
probe1start=270
probe1Stop=287
direction1=Forward
Tm1=69.05
score1=1.94
length=60

CT629
Nucleotide
Genomic coordinates:
Start: 247143
Stop: 244950 (SEQ ID NO: 274)

Amino Acid
MEGGDQRTKLTPATVMGLYQSKTPGEGEGGEGGGQFKIPSAIAVKSCCSKNATRRSPPSD
SPYSLRPMKRLKKNNGEVGGKAPPPVTLRLREDYESTPYNFNRNKKKRPITIDENQFATL
NPTYATDIIKKQQLPSVSAASVLRKHRANADTQYRKRFSHPNCAKFSTVNLKARDYTPLS
VLRSHVKGPKHLKSSCDTVTETNVVKRNFSSIDKWVKLEKPPCYFAVAEADTNIAAGLES
PFHLIRQAAKLGLISDVQDVSSNYETIKQSCIDAKEKASKFLWSNNRTKQPPSSWWPVGF
GSKNLSVLDTSPLLNWNRLCKNNGKGWIKTMSIDHMAKNVFKLSPGACESILEKKTTLLG
EVTAQCKKWESYRRNIPVPAHVQPEYASQVVMIGPSELYLEVKVGVYYMLETGKVIKFMT
DKEMYCEFVFETVFSHALEGRMKGAVGVRKMCVEGFCVEMDFAGISVIDVLNGDLKCKMD
ENVVQQPNPSTTSSKPAAELMQDHGSLCRMRDTLYGVRMLQATGRLPEGLQSKCKKPITD
SISAIAIVGKMRERMLNQLPFVLVEIVNIVTRLSQQGLVNPDIKSDNIVIDGITGQPKMI
DFGLIVPCKKYYNFKCWGTDERFFSNHPHTAPEFINSELCSETAMTFGLAYLLIDMLSIL
IKRTADLSANSIYTNIPFLSIVSKMYDQEKTNRPRAYEIAPVIGACFPFKDNIAKLFQSP
KHSLYSKKVK
(SEQ ID NO: 275)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
Q20443 (Q20443) PRK-2 PROTEIN	46	0.001
Q17735 (Q17735) SIMILAR TO PROTEIN KINASE	44	0.004
KPC1_LYTPI (Q25378) PROTEIN KINASE C (EC 2.7.1.-)	43	0.007
O01715 (O01715) PROTEIN KINASE C	43	0.010
O01716 (O01716) PROTEIN KINASE C (FRAGMENT)	43	0.010
Q21734 (Q21734) PUTATIVE RIBOSOMAL PROTEIN S6 KINASE II ALP	42	0.017

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 1 to 933 of CT629: this corresponds to nucleotides 244994 to 245926 of the genomic reference sequence.

TaqMan Primer/Probe Sets:
5'start=933
5'stop=954
3'start=1020
3'stop=1040
5'primer=CCCTCTCTTGAACTGGAACAGG (residues 933 to 954 of SEQ ID NO:274)
Tm5=58.83
3'primer=GCTCCAGGGGAAAGCTTAAAA (residues 1020 to 1040 of SEQ ID NO:274)
Tm3=58.49
probe1=TGAGCATCGATCACATGG (residues 992 to 1009 of SEQ ID NO:274)
probe1start=992
probe1Stop=1009
direction1=Forward
Tm1=68.98
score1=1.98
length=108

CT1030
Nucleotide
Genomic coordinates:
Start: 108549
Stop: 109164 (SEQ ID NO: 276)

Amino Acid
MSSGKVTYEIVEGGLLNNKYLLDGGAAICLQSNCVARKRHAGSLHDNLFKMLGFGDPYKQ
RRGKTNSKNLAIIEDRPQLGSVSVVQHPTEPERFCSMTFLFAQYNMGNGRKCYFPNDKEY
VESCKKHERVHKSSTEMKRLRLYYFNKCLHAIAKSPAMKKYNKIIFPARIGCAAAGGDWE
KYHASIRDFSTIIDKEVIIVSQRM
(SEQ ID NO: 277)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
Q9YTM9 (Q9YTM9) ORF 36	32	4.3
Q9XAQ7 (Q9XAQ7) NUOD, NADH DEHYDROGENASE SUBUNIT	31	9.7

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 1 to 604 of CT1030: this corresponds to nucleotides 108546 to 109149 of the genomic reference sequence.

TaqMan Primer/Probe Sets:
5'start=284
5'stop=307
3'start=387
3'stop=408
5'primer=GCTCCATGACATTCTTATTTGCTC (residues 284 to 307 of SEQ ID NO:276)
Tm5=57.98
3'primer=TTCTGTGGAAGATTTGTGGACC (residues 387 to 408 of SEQ ID NO:276)
Tm3=57.62
probe1=TGTTGAGAGCTGCAAGAA (residues 360 to 377 of SEQ ID NO:276)
probe1start=360
probe1Stop=377
direction1=Forward
Tm1=69.08
score1=1.91
length=125

CT1031
Nucleotide
Genomic coordinates:
Start: 109260
Stop: 110088 (SEQ ID NO: 278)

Amino Acid
MSSNRFSQLRGNEEMVGDYSRWTTVKNRRNRQQQYSHSFRPQQQQQHQKRTSTNSPPAPP
PPFPIISWGALGSYSMYRLDDQCRNCDETGYYNFHSYDRKRERVRSLNNTPSEGMWRRTS
RSSPFLNKKKDVDEAPPPQSNQHMYPLNKYSFREYTPSSKLVNWRDPSQEKQDKILQEEE
ARAPTPTPQEKEPEVETKDDVVIEEETAPEPEPEPAPVPDPDIPAITATTTTTTVATRHD
DSSTVFLRNVILSIVFWFLGVYSALFAKCIRSKKE
(SEQ ID NO: 279)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
Q01823 (Q01823) ORF-3	48	5e-05
PAR1_TRYBB (P08469) PROCYCLIC FORM SPECIFIC POLYPEPTIDE B1-	48	7e-05
Q99356 (Q99356) PROCYCLIN	48	9e-05
P73032 (P73032) HYPOTHETICAL 185.1 KD PROTEIN	48	9e-05
PARC_TRYBB (Q06084) PROCYCLIC FORM SPECIFIC POLYPEPTIDE B-A	48	9e-05
Q27045 (Q27045) SCHIZONT/SPOROZOITE SURFACE PROTEIN (FRAGME	48	9e-05

Comments:
EST confirmation of the predicted transcript:
An isolated EST has sequence identity to nucleotides 137 to 680 of CT1031: this corresponds to nucleotides 109401 to 109944 of the genomic reference sequence.

TaqMan Primer/Probe Sets:
5'start=255
5'stop=277
3'start=347
3'stop=364
5'primer=TTGCGATGAAACTGGCTATTACA (residues 255 to 277 of SEQ ID NO:278)
Tm5=58.44
3'primer=ATCTACTTGTGCGCCGCC (residues 347 to 364 of SEQ ID NO:278)
Tm3=58.42
probe1=CTCCAAGTGAAGGCATGT (residues 329 to 346 of SEQ ID NO:278)
probe1start=329
probe1Stop=346
direction1=Forward
Tm1=68.97
score1=1.97
length=110

CT1032
Nucleotide
Genomic coordinates:
Start: 119056
Stop: 121081 (SEQ ID NO: 280)

Amino Acid
MAGNRTQFVSSLIAKCISDVEQGMECCGRQAQDALMTRLANLKLGDSLKETDVNLEYLRY
ASTPLLGELNYDKQQYAATVDINLMAHFSYAALGIESILNSIRRVVVANHQRRNNGKKPS
EPISRPHPLGGVEPPLSSELANAIRDKFISMGALDRLNSAIVTAALGAIASERELFLREN
AVNYMYDVEFAERDAATTDTGNVVYLSTKMDEDEDDIIKRSEILDKVSKRPAKEGIDWRP
TPDNSFPYQLIWGDDSVDDTVLIDLITNAIVPNIFMAKFILFICNHLRAVIRSMREILYG
NISSSSDNYFEDGRKWCFWLNLYNRLEWFMLVVRFVIFLHSKKESFSGADNVNVKRLLVV
VVESFPPVLLDTEWVKTNITSWPVINNSNNNSTLPVTEDTLMRLAIRTSSGARHPIFDEI
NSLTTAVTNRITFQSAEFCTKILLGRALDEEEAGTKMLVKSVKETGEEKDKNNTFSSFGL
LLKNTKNEELEINIGDNDDETTDVACWARTSSTSFIRNRTYAFKKIWGLEDASDVVELKR
ESDAITSFVTDKSSPLLFPYVSDWSCLLLHPCCKAPAIIKSVWLQILKDFSQENIKTINE
KVQSLSSEICQKSNDRFKNKKIAAEHVRSVKKLLNTISNREQEAALSTEHCIWLTILWKQ
VVQNTLNLLENFPV
(SEQ ID NO: 281)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
O25761 (O25761) HYPOTHETICAL 88.8 KD PROTEIN	38	0.29
O75130 (O75130) KIAA0635 PROTEIN	34	3.3
Q17425 (Q17425) HYPOTHETICAL 62.4 KD PROTEIN B0024.10 IN CH	34	3.3
O33600 (O33600) PURINE NTPASE	34	4.4
Y066_NPVAC (P41467) HYPOTHETICAL 94.0 KD PROTEIN IN POL-LEF	34	4.4
Q53626 (Q53626) ATP-BINDING PROTEIN INVOLVED IN MITHRAMYCIN	33	5.7

Comments:

CT1033
Nucleotide
Genomic coordinates:
Start: 121099
Stop: 123634(SEQ ID NO: 282)

Amino Acid
MFTHLTRAFRKMNNLVNRSFIDVHRVVAELSYPEFEEDVKNPESSIYRTPISLFQNKDIV
TIVGDYILSPKTDSFQVLYPIKKVIEHFPVIFHCTHNNAPLWVHLLDERHHRLLQSLLTY
EIVNAKYRGIVVIPYYRRPINYQTGKSLLMSKLASVKVLDILMRCGSYKFISLMCMINKK
NNTNFLHCCASKWGEVGSKMMLHIAEMFFANPTTSQHLSDASSFPDAAAEDDKGKTPAHL
AIQEDNADALLFLISLYGAPWFQDNNSYMKSALELKSNKCVKVLSFAADKYEILPNINNN
QLEPDTMCGVCATSVEEDENEGKTTSLSWYQMNCKHYIHCECLMGMCAAAGNVQCPMCRE
DVGDEVLERCPPTIFRWLKLAERSEHNRVLFEAKKQEFYKQMEAMKPPRVVVPPRRTFLT
PARRGERAIRIAREIATNAIAEATAQGDVNSYFPVLIDGSGEEYEEEGEEFFNSEEEALA
FGRPFLEDEEEARQIQMRQFAELSRRGVSVNIINNDNPHRHISTVNIVQPVYGVEKSPAA
SFIYNMLKNDVFESIRSRDTRVGGERVPVMNLSNDKRALFHAASSMLCDFATETNSQIVG
LDFQAVYDPHHISNYIETFGSPLHAYPGAVTFLDGAQDYYAESIRYDNDIVSFSEMASEL
HITEALDVFEGSLLSPLFKKIRTGKSYSNWNDHLRRRNYARDIAEEFVRVCENSLASREH
PPVHVHPFRDGAIPILIEYIVDFIHHCITWSMQVNALHCMRKYIEHENTNVHLLNLRPTD
ERVEVLRVSQLRWSRLFNEQYNTRMSLSTKRLSLMKIFNHDLGVSKFGVYKLLDIIEMYC
FTLI
(SEQ ID NO: 283)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
Q9XUM8 (Q9XUM8) W02A11.3 PROTEIN	39	0.17
YEYC_CAEEL (Q21802) HYPOTHETICAL 64.6 KD PROTEIN R07B7.12 I	38	0.22
CAB40955 (CAB40955) HYPOTHETICAL 22.5 KD PROTEIN	37	0.50
YBR2_YEAST (P38239) HYPOTHETICAL 13.2 KD PROTEIN IN ORC2-TI	37	0.50
Q47955 (Q47955) HHDA PRECURSOR	37	0.50
O82239 (O82239) F17A22.9 PROTEIN	37	0.50

Comments:
EST confirmation of the predicted transcript:
An isolated EST has sequence identity to nucleotides 1 to 208 of CT1033: this corresponds to nucleotides 123449 to 123656 of the genomic reference sequence.

TaqMan Primer/Probe Sets:
5'start=1206
5'stop=1225
3'start=1269
3'stop=1287
5'primer=GGAAGCAATGAAACCTCCCA (residues 1206 to 1225 of SEQ ID NO:282)
Tm5=58.56
3'primer=GATGGCTCGTTCGCCTCTT (residues 1269 to 1287 of SEQ ID NO:282)
Tm3=58.97
probe1=TTGTTCCTCCTCGCAGGA (residues 1232 to 1249 of SEQ ID NO:282)
probe1start=1232
probe1Stop=1249
direction1=Forward
Tm1=68.99
score1=1.99
length=82

CT1034
Nucleotide
Genomic coordinates:
Start: 123757
Stop: 126556 (SEQ ID NO: 284)

Amino Acid
MAADLLELAIQETIQSELEEIADTEFLNYLPHKTGICEEAAANGRPYLPTLEMRNEVDHF
WSQDNRKLKLLGHFCGNLYVEAFIAGSIDAETCVGFLRSQATGLGYPLLKKLALIAREDK
SNTTNYNLYIDRNSMMKQVFSAEIDKRPSSIQNTSHTKSSPVYLKLIDRRTECLALDWLD
ASKRTAKEIGAARKVCFLQNLIVAILIPAYTETFVLDTGNELEQQVLDDAYFNAENKDKV
DEMCVVAILSTLHNLFVRKSLPHHLYNAPFRLPPFGQHPIINIENSSFFNEDTTPILASI
SIPSSMVIKHHTRKNSRWRCPNNLMTAAERSIFLRGVLTVSGDYGWFSVIVGSTIMPSVL
FYGDRKHLINTVKSNNFSAITCSYWNKYMDCRSYGFEIIDTPENNCGFRIRAAIDCSNTD
FHSPVTRVNKKKTSIINAVKNPFFIRHTEPKWYNKNAMCGEVLENVGVTLEQHVRVSDEY
MDRFGSLLLGREKKWTCNYLDRIKSLETISNNLKGKIDTMCKILETKYNYKSSSLYYKQI
TATSDDPIKMKIIASINKRRYLCNILEFAIISSEKKDEVEEDHTKTGNGGCAFSKYKKKQ
LEPKQHLIVKVNKYIEAFSLIKMLRNDCERNKCRFKEAEIRECANELVRELYRASARSYV
HDLVLKRTNVHLTWQRPYDENANTIMSLIPKCKLHTVLYDKDSRDVKLLNFLRTRDGNYN
PIRHSMLELVYGEEYAKDVSTVTCFEWLKWCSKKGVIKYEDFLDRYEKTGEEDKDEREFF
RLKKCSRDHTKDIKKIENVLNSDTLYSYSLDKNVQTHASSSTVVKNDTDGKTSMVGWDYI
FSIGKGEKTTKKRKLETIDISSSDDDDEEEEEEDEGKRMKMNNCSSSIKNKSKNKNGRMC
CTDILNVVEPSLPNTLSFNCVKSMDVLNLL
(SEQ ID NO: 285)

Top Blast Hits

Sequences producing significant alignments:	Score (bits)	E Value
O62235 (O62235) F36F2.3 PROTEIN	46	8e-04
AAF04442 (AAF04442) PUTATIVE TRANSLATION INITIATION FACTOR	43	0.012
O60313 (O60313) KIAA0567 PROTEIN (FRAGMENT)	41	0.037
Q90491 (Q90491) DNA BINDING PROTEIN E12	41	0.048
BAA82145 (BAA82145) MYOSIN HEAVY CHAIN 2B	40	0.063
O97303 (O97303) PFC1060C PROTEIN	40	0.063

Comments:
EST confirmation of the predicted transcript:
An isolated EST has equence identity to nucleotides 1 to 647 of CT1034: this corresponds to nucleotides 125649 to 126295 of the genomic reference sequence.

TaqMan Primer/Probe Sets:
5'start=1391
5'stop=1410
3'start=1468
3'stop=1489
5'primer=AAAATGTTGGCGTGACCCTC (residues 1391 to 1410 of SEQ ID NO:284)
Tm5=58.49
3'primer=ACGTCCATTTCTTTTCTCGTCC (residues 1468 to 1489 of SEQ ID NO:284)
Tm3=58.24
probe1=AACAACACGTCCGTGTTA (residues 1412 to 1429 of SEQ ID NO:284)
probe1start=1412
probe1Stop=1429
direction1=Reverse
Tm1=69.00
score1=1.99
length=99

SBV.ORF022.txt
Nucleotide
Genomic Coordinates:
Start: 265664
Stop: 266297 (SEQ ID NO:286)

Comments: EST confirmation of transcript not predicted computationally.

TaqMan Primer/Probe Sets:
5'start=230
5'stop=252
3'start=321
3'stop=343
5'primer=CAAATCAAAGGCCATATGAAACC (residues 230 to 252 of SEQ ID NO:286)
Tm5=58.41
3'primer=GGTGGTCTTTATTTTCATCACCG (residues 321 to 343 of SEQ ID NO:286)
Tm3=58.41
primerScore=0.86
allele1=
probe1=GAGGATAGCCAGTTCTAT (residues 265 to 282 of SEQ ID NO:286)
probe1start=265
probe1Stop=282
direction1=Reverse
Tm1=68.99
score1=1.99
length=114

C003
Nucleotide
Genomic Coordinates:
Start: 126709
Stop: 127126 (SEQ ID NO: 287)

Comments: EST confirmation of transcript not predicted computationally.

TaqMan Primer/Probe Sets:
5'start=175
5'stop=194
3'start=265
3'stop=283
5'primer=CATGGTGTGCCTAAAGCAGG (residues 175 to 194 of SEQ ID NO:287)
Tm5=57.84
3'primer=TGGCACAATCATGGGTTGA (residues 265 to 283 of SEQ ID NO:287)
Tm3=57.81
primerScore=0.91
allele1=
probe1=AATGGAGGCATCGAAGAA (residues 212 to 229 of SEQ ID NO:287)
probe1start=212
probe1Stop=229
direction1=Reverse
Tm1=69.02
score1=1.97
length=109

C010
Nucleotide
Genomic Coordinates:
Start: 184094
Stop: 184931 (SEQ ID NO: 288)

Comments: EST confirmation of transcript not predicted computationally.

TaqMan Primer/Probe Sets:
5'start=547
5'stop=570
3'start=655
3'stop=678
5'primer=AAGATGATGAAACCTGGTTCAAAA (residues 547 to 570 of SEQ ID NO:288)
Tm5=57.75
3'primer=CGTCATGGAAGAAAAGGAATTGTA (residues 655 to 678 of SEQ ID NO:288)
Tm3=58.24
primerScore=0.67
allele1=
probe1=CTCCTTGCAAGTGCGATA (residues 598 to 615 of SEQ ID NO:288)
probe1start=598
probe1Stop=615
direction1=Forward
Tm1=69.01
score1=1.98
length=132

C020
Nucleotide
Genomic Coordinates:
Start: 60122
Stop: 60341 (SEQ ID NO: 289)

Comments: EST confirmation of transcript not predicted computationally.

TaqMan Primer/Probe Sets:
5'start=2
5'stop=26
3'start=118
3'stop=140
5'primer=CAACCTCCACATCTCCTTCTAATTC (residues 2 to 26 of SEQ ID NO: 289)
Tm5=58.27
3'primer=AACGCTTTGTTTAACGTGCTTTT (residues 118 to 140 of SEQ ID NO: 289)
Tm3=58.18
primerScore=0.61
allele1=
probe1=ATTCAAGAGGTCACAAACA (residues 80 to 98 of SEQ ID NO: 289)
probe1start=80
probe1Stop=98
direction1=Forward
Tm1=68.75
score1=1.50
length=139

C028
Nucleotide
Genomic Coordinates:
Start: 277009
Stop: 277324 (SEQ ID NO: 290)

Comments: EST confirmation of transcript not predicted computationally.

TaqMan Primer/Probe Sets:
5'start=293
5'stop=315
3'start=384
3'stop=406
5'primer=GGTGCAGTTTCATCCTTACCATT (residues 293 to 315 of SEQ ID NO: 290)
Tm5=58.07
3'primer=TCGTCATCATAGTCGTCGTCAAC (residues 384 to 406 of SEQ ID NO: 290)
Tm3=58.72
primerScore=0.86
allele1=
probe1=TTCCACAACCACCACTAC (residues 320 to 337 of SEQ ID NO: 290)
probe1start=320
probe1Stop=337
direction1=Forward
Tm1=68.94
score1=1.94
length=114

C036
Nucleotide
Genomic Coordinates:
Start: 115067 (SEQ ID NO: 291)
Stop: 115380

Comments: EST confirmation of transcript not predicted computationally.

TaqMan Primer/Probe Sets:
5'start=99
5'stop=117
3'start=158
3'stop=177
5'primer=CCACTGCTGGACGCATCTC (residues 99 to 117 of SEQ ID NO:291)
Tm5=58.94
3'primer=CGACGGACAGTGGAGCTCTT (residues 158 to 177 of SEQ ID NO: 291)
Tm3=59.04
primerScore=1.25
allele1=
probe1=CCATCAATGAAGAAGCGT (residues 131 to 148 of SEQ ID NO: 291)
probe1start=131
probe1Stop=148
direction1=Forward
Tm1=68.97
score1=1.97
length=79

C037
Nucleotide
Genomic Coordinates:
Start: 186828
Stop: 187047 (SEQ ID NO: 292)

Comments: EST confirmation of transcript not predicted computationally.

TaqMan Primer/Probe Sets:
5'start=63
5'stop=82
3'start=133
3'stop=157
5'primer=TTGACATCAGACCGACCCAG (residues 63 to 82 of SEQ ID NO: 292)
Tm5=58.08
3'primer=GGAATTTTACTCTTCCTCCATCTCA (residues 133 to 157 of SEQ ID NO: 292)
Tm3=57.92
primerScore=0.62
allele1=
probe1=CACCCTCTAAACTCGAGC (residues 88 to 105 of SEQ ID NO: 292)
probe1start=88
probe1Stop=105
direction1=Forward
Tm1=69.49
score1=1.50
length=95

C019
Nucleotide
Genomic Coordinates:
Start:141541
Stop: 141647 (SEQ ID NO: 293)

Comments: EST confirmation of transcript not predicted computationally.